

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 20:26:59 ; Search time 189 Seconds

(without alignments)
169.292 Million cell updates/sec

Title: US-10-727-358-5

Percent score: 18

Scoring table: IDENTITY NUC

Gapop 10-0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents NA.*

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2: /cgn2_6/ptodata/1/ina/5.COMB.seq:*
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9: /cgn2_6/ptodata/1/ina/backfillseq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match Length	ID	Description
1	18	100.0	4094 2	US-08-571-758-5
2	18	100.0	4094 2	US-08-909-984A-5
3	18	100.0	4094 2	US-08-909-983-5
4	15.4	85.6	543 3	US-09-621-976-17349
5	15.4	85.6	29889 3	US-09-949-016-13682
6	15.4	85.6	97195 3	US-09-949-016-12212
7	15.4	85.6	97196 3	US-09-949-016-16971
8	15	83.3	50 3	US-10-131-827-7589
9	15	83.3	3	US-09-513-999C-28900
10	15	83.3	783 3	US-09-157-910-6
11	15	83.3	868 3	US-09-484-970B-159
12	15	83.3	2399 3	US-09-023-655-508
13	14.8	82.2	601 3	US-09-949-016-23074
14	14.8	82.2	601 3	US-09-949-016-16971
15	14.8	82.2	2846 2	US-08-571-758-7
16	14.8	82.2	2846 2	US-08-909-984A-7
17	14.8	82.2	2846 2	US-08-909-983-7
18	14.8	82.2	3469 2	US-09-560-385A-23
19	14.8	82.2	3511 3	US-09-560-385A-21
20	14.8	82.2	3585 3	US-09-560-385A-19
21	14.8	82.2	3621 3	US-09-560-385A-17
22	14.8	82.2	3759 3	US-09-560-385A-15
23	14.8	82.2	3930 3	US-09-560-385A-13
24	14.8	82.2	3931 2	US-08-144-121-1

25	14.8	82.2	3931 2	US-08-735-893-1	Sequence 1, Appli
26	14.8	82.2	3931 3	US-10-841-139-1	Sequence 1, Appli
27	14.8	82.2	3971 3	US-09-876-176-1	Sequence 1, Appli
28	14.8	82.2	4108 3	US-09-919-172-15	Sequence 15, Appli
29	14.8	82.2	17410 2	US-07-841-646-3	Sequence 3, Appli
30	14.8	82.2	17410 2	US-08-147-023-3	Sequence 3, Appli
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32	14.8	82.2	17410 2	US-08-449-700-3	Sequence 3, Appli
33	14.8	82.2	17410 2	US-08-449-699A-3	Sequence 3, Appli
34	14.8	82.2	17410 3	US-09-148-925C-3	Sequence 3, Appli
35	14.8	82.2	17410 3	US-08-957-425-3	Sequence 3, Appli
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37	14.8	82.2	17415 3	US-08-486-343A-1	Sequence 1, Appli
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39	14.8	82.2	17415 6	PCT-US95-07349-1	Sequence 1, Appli
40	14.8	82.2	99748 3	US-09-949-016-11990	Sequence 11990, A
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42	14.4	80.0	364 3	US-09-513-999C-26439	Sequence 26439, A
43	14.4	80.0	658 3	US-09-641-638-402	Sequence 402, App
44	14.4	80.0	658 3	US-10-170-097-402	Sequence 402, App
45	14.4	80.0	939 3	US-09-641-638-403	Sequence 403, App
46	14.4	80.0	939 3	US-10-170-097-403	Sequence 403, App
47	14.4	80.0	1022 3	US-09-257-584-5	Sequence 5, Appli
48	14.4	80.0	3153 3	US-08-110-047-127	Sequence 327, App
49	14.4	80.0	8333 2	US-08-110-300A-8	Sequence 8, Appli
50	14.4	80.0	8333 2	US-08-886-642-8	Sequence 8, Appli
51	14.4	80.0	8333 3	US-09-433-322B-2	Sequence 2, Appli
52	14.4	80.0	8333 3	US-09-970-597-2	Sequence 2, Appli
53	14.4	80.0	8323 6	PCT-US93-08041-8	Sequence 8, Appli
54	14.4	80.0	10367 2	US-08-110-300A-9	Sequence 9, Appli
55	14.4	80.0	10367 2	US-08-886-642-9	Sequence 9, Appli
56	14.4	80.0	10367 6	PCT-US93-08041-9	Sequence 9, Appli
57	14.4	80.0	18443 3	US-09-078-294-6	Sequence 6, Appli
58	14	77.8	616 3	US-09-533-559-2321	Sequence 2321, Appli
59	14	77.8	5706 3	US-09-270-767-12590	Sequence 12590, A
60	14	21105 3	US-09-949-016-15722	Sequence 15722, A	
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62	13.8	76.7	20 3	US-09-198-452A-5583	Sequence 5583, Appli
63	13.8	76.7	235 3	US-09-513-999C-17184	Sequence 17184, A
64	13.8	76.7	302 2	US-08-849-701-3	Sequence 3, Appli
65	13.8	76.7	459 3	US-09-513-999C-24323	Sequence 24323, A
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69	13.8	76.7	601 3	US-09-949-016-27115	Sequence 27115, A
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71	13.8	76.7	601 3	US-09-949-016-32557	Sequence 32557, A
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87	13.8	76.7	601 3	US-09-949-016-177418	Sequence 177418, A
88	13.8	76.7	601 3	US-09-949-016-182373	Sequence 182373, A
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91	13.8	76.7	601 3	US-09-949-016-182901	Sequence 182901, A
92	13.8	76.7	601 3	US-09-949-016-196347	Sequence 196347, A
93	13.8	76.7	604 3	US-09-974-528-233	Sequence 233, App
94	13.8	76.7	604 3	US-10-120-988-233	Sequence 233, App
95	13.8	76.7	616 3	US-09-465-558-15	Sequence 15, Appli
96	13.8	76.7	629 3	US-09-270-767-6755	Sequence 6755, Appli
97	13.8	76.7	629 3	US-09-270-767-22037	Sequence 22037, Appli

98	13.8	76.7	763	3	US-09-586-106D-138	Sequence 118, App	C 171	13.8	76.7	44120	3	US-09-949-016-14154	Sequence 14154, A
99	13.8	76.7	763	3	US-10-799-870-138	Sequence 118, App	C 172	13.8	76.7	44120	3	US-09-949-016-14155	Sequence 14155, A
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101	13.8	76.7	818	3	US-09-020-956-27	Sequence 27, Appl	C 174	13.8	76.7	44676	3	US-09-949-016-17511	Sequence 17511, A
102	13.8	76.7	818	3	US-09-030-607-27	Sequence 27, Appl	C 175	13.8	76.7	51967	3	US-09-949-016-16582	Sequence 16582, A
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109	13.8	76.7	818	3	US-09-115-453-27	Sequence 27, Appl	C 182	13.8	76.7	66213	3	US-09-949-016-16739	Sequence 16739, A
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112	13.8	76.7	818	3	US-09-759-143-27	Sequence 27, Appl	C 185	13.8	76.7	72742	3	US-09-949-016-16161	Sequence 16161, A
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114	13.8	76.7	818	3	US-09-030-606-27	Sequence 27, Appl	C 187	13.8	76.7	87734	3	US-09-949-016-17521	Sequence 17521, A
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121	13.8	76.7	1351	2	US-09-016-434-1303	Sequence 1303, Ap	C 194	13.8	76.7	109025	3	US-09-949-016-17534	Sequence 17534, A
122	13.8	76.7	1457	3	US-09-673-395A-554	Sequence 554, App	C 195	13.8	76.7	109025	3	US-09-949-016-17567	Sequence 17567, A
123	13.8	76.7	1559	3	US-09-482-273-56	Sequence 56, Appl	C 196	13.8	76.7	110243	3	US-09-949-016-13598	Sequence 13598, A
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167	13.8	76.7	39498	3	US-09-949-016-16505	Sequence 16505, A	C 240	13.4	74.4	530	3	US-09-949-016-13209	Sequence 13209, A
168	13.8	76.7	44120	3	US-09-949-016-14151	Sequence 14151, A	C 241	13.4	74.4	530	3	US-09-949-016-13209	Sequence 13209, A
169	13.8	76.7	44120	3	US-09-949-016-14152	Sequence 14152, A	C 242	13.4	74.4	530	3	US-09-949-016-13209	Sequence 13209, A
170	13.8	76.7	44120	3	US-09-949-016-14153	Sequence 14153, A	C 243	13.4	74.4	530	3	US-09-949-016-13209	Sequence 13209, A

244 13.4 74.4 681 3 US-09-774-528-62 Sequence 62, Appl
245 13.4 74.4 681 3 US-10-120-988-62 Sequence 62, Appl
246 13.4 74.4 700 3 US-09-244-805-46 Sequence 46, Appl
247 13.4 74.4 988 3 US-09-533-559-1995 Sequence 45, Appl
248 13.4 74.4 1210 3 US-09-244-805-45 Sequence 6, Appl
249 13.4 74.4 1230 3 US-09-244-805-6 Sequence 1237, Ap
250 13.4 74.4 1497 3 US-09-949-016-1237 Sequence 344, App
251 13.4 74.4 2496 3 US-10-104-047-344 Sequence 12381, A
252 13.4 74.4 11089 3 US-09-949-016-12381 Sequence 13791, A
253 13.4 74.4 11113 3 US-09-949-016-13791 Sequence 17225, A
254 13.4 74.4 15543 3 US-09-949-016-17225 Sequence 14710, A
255 13.4 74.4 16520 3 US-09-949-016-14710 Sequence 15394, A
256 13.4 74.4 16520 3 US-09-949-016-15394 Sequence 17291, A
257 13.4 74.4 16782 3 US-09-949-016-17291 Sequence 12506, A
258 13.4 74.4 19728 3 US-09-949-016-12506 Sequence 15767, A
259 13.4 74.4 19728 3 US-09-949-016-15767 Sequence 12979, A
260 13.4 74.4 24715 3 US-09-949-016-12979 Sequence 16841, A
261 13.4 74.4 26103 3 US-09-949-016-16841 Sequence 12826, A
262 13.4 74.4 26967 3 US-09-949-016-12926 Sequence 17062, A
263 13.4 74.4 29516 3 US-09-949-016-17062 Sequence 12625, A
264 13.4 74.4 29763 3 US-09-949-016-12625 Sequence 15395, A
265 13.4 74.4 30371 3 US-09-949-016-15395 Sequence 14319, A
266 13.4 74.4 31391 3 US-09-949-016-14319 Sequence 16382, A
267 13.4 74.4 36103 3 US-09-949-016-16382 Sequence 1, Appl
268 13.4 74.4 43804 3 US-09-970-711-1 Sequence 1, Appl
269 13.4 74.4 43804 3 US-09-970-711-1 Sequence 13191, A
270 13.4 74.4 57002 3 US-09-949-016-13191 Sequence 1, Appl
271 13.4 74.4 81001 3 US-09-750-580-1 Sequence 1568, A
272 13.4 74.4 91772 3 US-09-949-016-15568 Sequence 17433, A
273 13.4 74.4 101349 3 US-09-949-016-17433 Sequence 1648, A
274 13.4 74.4 101951 3 US-09-949-016-15648 Sequence 38, Appl
275 13.4 74.4 128779 3 US-09-497-855A-38 Sequence 12544, A
276 13.4 74.4 129380 3 US-09-949-016-12544 Sequence 15617, A
277 13.4 74.4 135171 3 US-09-949-016-15617 Sequence 15238, A
278 13.4 74.4 143644 3 US-09-949-016-15238 Sequence 11989, A
279 13.4 74.4 158735 3 US-09-949-016-11989 Sequence 17130, A
280 13.4 74.4 158735 3 US-09-949-016-17130 Sequence 14264, A
281 13.4 74.4 162465 3 US-09-949-016-14264 Sequence 15999, A
282 13.4 74.4 169334 3 US-09-949-016-15999 Sequence 12776, A
283 13.4 74.4 187169 3 US-09-949-016-12776 Sequence 13266, A
284 13.4 74.4 187580 3 US-09-949-016-13266 Sequence 15546, A
285 13.4 74.4 187580 3 US-09-949-016-15546 Sequence 12111, A
286 13.4 74.4 187595 3 US-09-949-016-12111 Sequence 15940, A
287 13.4 74.4 187848 3 US-09-949-016-15940 Sequence 12968, A
288 13.4 74.4 191569 3 US-09-949-016-12968 Sequence 15725, A
289 13.4 74.4 222452 3 US-09-949-016-15725 Sequence 15297, A
290 13.4 74.4 264358 3 US-09-949-016-15297 Sequence 14578, A
291 13.4 74.4 421118 3 US-09-949-016-14577 Sequence 9726, Ap
292 13.4 74.4 678533 3 US-09-949-016-14578 Sequence 1222, Ap
293 13.4 74.4 678533 3 US-09-949-016-14578 Sequence 4036, Ap
294 13.2 73.3 205 3 US-09-513-999C-9726 Sequence 5310, Ap
295 13.2 73.3 272 3 US-09-313-294A-1222 Sequence 21192, A
296 13.2 73.3 294 3 US-09-313-294A-4036 Sequence 10057, A
297 13.2 73.3 295 3 US-09-270-767-5910 Sequence 4092, Ap
298 13.2 73.3 295 3 US-09-270-767-21192 Sequence 4092, Ap
299 13.2 73.3 382 3 US-09-513-999C-10057 Sequence 4092, Ap
300 13.2 73.3 384 3 US-09-252-991A-4092

ALIGNMENTS

RESULT 1
US-08-571-758-5
Sequence 5, Application US/08571758
Patent No. 570675
GENERAL INFORMATION:
APPLICANT: Rubin, Gerry M.
APPLICANT: Therrien, Marc
APPLICANT: Chang, Henry C.
APPLICANT: Karim, Felix D.
APPLICANT: Massarman, David A.
TITLE OF INVENTION: A No. 570675e1 Protein Kinase Required for Ras

TITLE OF INVENTION: Signal Transduction
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/571,758
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4094 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-571-758-5
Query Match 100.0%; Score 18; DB 2; Length 4094;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGACCTAGAGGCAAG 18
Db 296 CGGACCTAGAGGCAAG 313
RESULT 2
US-08-909-984A-5
Sequence 5, Application US/0890984A
Patent No. 5747275
GENERAL INFORMATION:
APPLICANT: Rubin, Gerry M.
APPLICANT: Therrien, Marc
APPLICANT: Chang, Henry C.
APPLICANT: Karim, Felix D.
APPLICANT: Massarman, David A.
TITLE OF INVENTION: A No. 5747275e1 Protein Kinase Required for Ras
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,984A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4341
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4094 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-909-983A-5

Query Match 100.0%; Score 18; DB 2; Length 4094;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGACCCCTAGAGGCAAG 18
Db 296 CGACCCCTAGAGGCAAG 313

RESULT 3
US-08-909-983-5
Sequence 5, Application US/08909983
Patent No. 5747288
GENERAL INFORMATION:
APPLICANT: Rubin, Gerry M.
APPLICANT: Therrien, Marc
APPLICANT: Chang, Henry C.
APPLICANT: Karim, Felix D.
APPLICANT: Massarman, David A.
TITLE OF INVENTION: A No. 5747288el Protein Kinase Required for Ras
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,983
FILING DATE: 12-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/571,758
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4341
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4094 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-909-983-5

Query Match 100.0%; Score 18; DB 2; Length 4094;

Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGACCCCTAGAGGCAAG 18
Db 296 CGACCCCTAGAGGCAAG 313

RESULT 4
US-09-621-976-17349/C
Sequence 17349, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSER 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 17349
LENGTH: 543
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-17349

Query Match 85.6%; Score 15.4; DB 3; Length 543;
Best Local Similarity 94.1%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GACCCCTAGAGGCAAG 18
Db 488 GACCCCTAGAGGCAAG 472

RESULT 5
US-09-949-016-13682
Sequence 13682, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13682
LENGTH: 29889
TYPE: DNA
ORGANISM: Human
US-09-949-016-13682

Query Match 85.6%; Score 15.4; DB 3; Length 29889;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GACCCCTAGAGGCAAG 18
Db 29541 GACCCCTAGAGGCAAG 29557

RESULT 6
US-09-949-016-12212/C

Sequence 12212, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12212
LENGTH: 97195
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1) ..(97195)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12212

Query Match 85.6%; Score 15.4; DB 3; Length 97195;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTTAGAGGCAAG 18
DB 77970 GGACCTTAGAGGCAAG 77954

RESULT 7
US-09-949-016-16971/c
Sequence 16971, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16971
LENGTH: 97196
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1) ..(97196)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16971

Query Match 85.6%; Score 15.4; DB 3; Length 97196;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTTAGAGGCAAG 18
DB 77970 GGACCTTAGAGGCAAG 77954

RESULT 8
US-10-131-827-7589
Sequence 7589, Application US/10131827
Patent No. 6905827
GENERAL INFORMATION:
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMM
FILE REFERENCE: 50661200120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7589
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-7589

Query Match 83.3%; Score 15; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GGACCTTAGAGGCA 16
DB 18 GGACCTTAGAGGCA 32

RESULT 9
US-09-513-999C-28900
Sequence 28900, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59 US2 REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 28900
LENGTH: 163
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-28900

Query Match 83.3%; Score 15; DB 3; Length 163;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GGACCTTAGAGGCA 16
DB 148 GGACCTTAGAGGCA 162

RESULT 10
US-09-157-910-6
Sequence 6, Application US/09157910A
Patent No. 6197744
GENERAL INFORMATION:

APPLICANT: Berleth, Erica
APPLICANT: Burke, M. Jane
APPLICANT: Nadadur, Srikanth
APPLICANT: Gurtoo, Hira
APPLICANT: Henn, Alicia
APPLICANT: Minich, Enrico
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitory Protein TIP-B1 and Method
TITLE OF INVENTION: of Using Same
FILE REFERENCE: RPP:151-US
CURRENT APPLICATION NUMBER: US/09/157,910A
CURRENT FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Microsoft Word 97 / MS-DOS Ver. 7.10
SEQ ID NO 6
LENGTH: 783
TYPE: DNA
ORGANISM: HOMO SAPIENS
FEATURE:
OTHER INFORMATION: This sequence encodes the TIP-B1 peptides of SEQ. ID. #3,
OTHER INFORMATION: SEQ. ID. #4 and SEQ. ID. #5
US-09-157-910-6

Query Match 83.3%; Score 15; DB 3; Length 783;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GGACCTAGAGGCAA 16
Db 730 GGACCTAGAGGCAA 744

RESULT 11
US-09-484-9708-159
Sequence 159, Application US/094849708
Patent No. 6426186
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Volkmutch, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 159
LENGTH: 868
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6426186 234571.8
NAME/KEY: unsure
LOCATION: 23, 27
OTHER INFORMATION: a, c, g, or other
US-09-484-9708-159

Query Match 83.3%; Score 15; DB 3; Length 868;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GGACCTAGAGGCAA 16
Db 820 GGACCTAGAGGCAA 834

RESULT 12
US-09-023-655-508
Sequence 508, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocker, Benjamin G.
APPLICANT: Susan G. Stuart

APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 508:
SEQUENCE CHARACTERISTICS:
LENGTH: 2399 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: MPMGNOT02
CLONE: 201392
US-09-023-655-508

Query Match 83.3%; Score 15; DB 3; Length 2399;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GGACCTAGAGGCAA 16
Db 2294 GGACCTAGAGGCAA 2308

RESULT 13
US-09-949-016-23074/C
Sequence 23074, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23074
LENGTH: 601
TYPE: DNA

ORGANISM: Human
US-09-949-016-23074

Query Match 82.2%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGACCTTAGGCGCAAG 18
Db 190 CAGACCTTAGGCGCAAG 173

RESULT 14
US-09-949-016-169781/c
Sequence 169781, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 169781
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-169781

Query Match 82.2%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGACCTTAGGCGCAAG 18
Db 190 CAGACCTTAGGCGCAAG 173

RESULT 15
US-08-571-758-7
Sequence 7, Application US/08571758
Patent No. 570675

GENERAL INFORMATION:
APPLICANT: Rubin, Gerry M.
APPLICANT: Therrien, Marc
APPLICANT: Chang, Henry C.
APPLICANT: Karim, Felix D.
APPLICANT: Wasserman, David A.
TITLE OF INVENTION: A No. 570675el Protein Kinase Required for Ras
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/571,758

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2846 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-571-758-7

Query Match 82.2%; Score 14.8; DB 2; Length 2846;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGACCTTAGGCGCAAG 18
Db 214 CAGACCTTAGGCGCAAG 231

RESULT 16
US-08-909-984A-7
Sequence 7, Application US/08909984A
Patent No. 5747275

GENERAL INFORMATION:
APPLICANT: Rubin, Gerry M.
APPLICANT: Therrien, Marc
APPLICANT: Chang, Henry C.
APPLICANT: Karim, Felix D.
APPLICANT: Wasserman, David A.
TITLE OF INVENTION: A No. 5747275el Protein Kinase Required for Ras
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,984A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2846 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-909-984A-7

Query Match 82.2%; Score 14.8; DB 2; Length 2846;

Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CGGACCTTAGAGGCAAG 18
Db 214 CGGACCTTAGAGGCAAG 231

RESULT 17
US-08-909-983-7
Sequence 7, Application US/08909983
Patent No. 5747288
GENERAL INFORMATION:
APPLICANT: Rubin, Gerry M.
APPLICANT: Therien, Marc
APPLICANT: Chang, Henry C.
APPLICANT: Karim, Felix D.
APPLICANT: Massam, David A.
TITLE OF INVENTION: A No. 5747288el Protein Kinase Required for Ras
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,983
FILING DATE: 12-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/571,758
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-010
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2846 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-909-983-7
Query Match 82.2%; Score 14.8; DB 2; Length 2846;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CGGACCTTAGAGGCAAG 18
Db 214 CGGACCTTAGAGGCAAG 231

RESULT 18
US-09-560-385A-23
Sequence 23, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Bouland, Ariel
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C

CURRENT APPLICATION NUMBER: US/09/560,385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 3469
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(3465)
US-09-560-385A-23

Query Match 82.2%; Score 14.8; DB 3; Length 3469;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CGGACCTTAGAGGCAAG 18
Db 1816 CGGACCTTAGAGGCAAG 1833

RESULT 19
US-09-560-385A-19
Sequence 19, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Bouland, Ariel
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560,385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 3511
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (7)..(3507)
NAME/KEY: misc_feature
LOCATION: (13)..(36)
US-09-560-385A-19

Query Match 82.2%; Score 14.8; DB 3; Length 3511;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CGGACCTTAGAGGCAAG 18
Db 1858 CGGACCTTAGAGGCAAG 1875

RESULT 20
US-09-560-385A-21
Sequence 21, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Bouland, Ariel
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560,385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 3585
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (60)..(3581)

NAME/KEY: sig_peptide
LOCATION: (60)..(116)
US-09-560-385A-21

Query Match
Best Local Similarity 82.2%; Score 14.8; DB 3; Length 3585;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18
DB 1932 CGGATCCTAGATGCAAG 1949

RESULT 21
US-09-560-385A-17
Sequence 17, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Boulard, Ariel
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560.385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 3621
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (60)..(3617)
NAME/KEY: sig_peptide
LOCATION: (60)..(110)
NAME/KEY: misc feature
LOCATION: (123)..(146)
US-09-560-385A-17

Query Match
Best Local Similarity 82.2%; Score 14.8; DB 3; Length 3621;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18
DB 1968 CGGATCCTAGATGCAAG 1985

RESULT 22
US-09-560-385A-15
Sequence 15, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Boulard, Ariel
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560.385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 3759
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (11)..(1459)
US-09-560-385A-15

Query Match
Best Local Similarity 82.2%; Score 14.8; DB 3; Length 3759;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18

DB 1810 CGGATCCTAGATGCAAG 1827

RESULT 23
US-09-560-385A-13
Sequence 13, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Boulard, Ariel
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560.385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 3930
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (121)..(3630)
NAME/KEY: sig_peptide
LOCATION: (121)..(171)
US-09-560-385A-13

Query Match
Best Local Similarity 82.2%; Score 14.8; DB 3; Length 3930;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18
DB 1981 CGGATCCTAGATGCAAG 1998

RESULT 24
US-08-144-121-1
Sequence 1, Application US/08144121
Patent No. 5610031
GENERAL INFORMATION:
APPLICANT: Burgeson, Robert E.
APPLICANT: Magman, David W.
TITLE OF INVENTION: BIK CHAIN OF LAMININ AND METHODS OF USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: BOSTON
STATE: Massachusetts
COUNTRY: United States
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/144,121
FILING DATE: 27-OCT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: (MCH-0780.0) MGP-021
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3931 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 122..3617
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 173..3617
US-08-144-121-1

Query Match 82.2%; Score 14.8; DB 2; Length 3931;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGACCTAGAGGCAAG 18
Db 1976 CGGATCCTAGATGCAAG 1993

RESULT 25

US-08-735-893-1

Sequence 1, Application US/08735893

Patent No. 5914317

GENERAL INFORMATION:

APPLICANT: Burgesson, Robert E.

APPLICANT: Wagsman, David W.

TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, suite 510

CITY: BOSTON

STATE: Massachusetts

COUNTRY: United States

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/735,893

FILING DATE: 18-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/144,121

FILING DATE: 27-OCT-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Paul L.

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: (MCH-0780.1) MGP-021DV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3931 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 122..3617

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 173..3617

US-08-735-893-1

Query Match 82.2%; Score 14.8; DB 2; Length 3931;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGACCTAGAGGCAAG 18
Db 1976 CGGATCCTAGATGCAAG 1993

RESULT 26

US-10-841-139-1

Sequence 1, Application US/10841139

Patent No. 6916631

GENERAL INFORMATION:

APPLICANT: Burgesson, Robert E.

APPLICANT: Wagsman, David W.

TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE

FILE REFERENCE: 10287/021003

CURRENT FILING DATE: 2004-05-07

PRIOR FILING DATE: 2003-05-22

PRIOR APPLICATION NUMBER: US/09/161,872

PRIOR FILING DATE: 1998-09-28

PRIOR APPLICATION NUMBER: US 08/735,893

PRIOR FILING DATE: 1996-10-23

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 3931

TYPE: DNA

ORGANISM: Homo sapiens

NAME/KEY: CDS

LOCATION: (122)..(3616)

FEATURE:

NAME/KEY: mat_peptide

LOCATION: (173)..(3616)

US-10-841-139-1

Query Match 82.2%; Score 14.8; DB 3; Length 3931;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGACCTAGAGGCAAG 18
Db 1976 CGGATCCTAGATGCAAG 1993

RESULT 27

US-09-876-176-1

Sequence 1, Application US/09876176

Patent No. 6586244

GENERAL INFORMATION:

APPLICANT: Reinhard, Christoph

APPLICANT: Jefferson, Anne B.

APPLICANT: Den-Otter, Douglas R.

APPLICANT: Winter, Jill A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

FILE REFERENCE: PP-01702.002/200130.523

CURRENT FILING DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 3971

TYPE: DNA

ORGANISM: Homo sapiens

US-09-876-176-1

Query Match 82.2%; Score 14.8; DB 3; Length 3971;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGACCTAGAGGCAAG 18

Db 1948 CGATCCTGATGCAAG 1965

RESULT 28

US-09-919-172-15
Sequence 15, Application US/09919172

Patent No. 6673545

GENERAL INFORMATION:

APPLICANT: Fakis, Mary

APPLICANT: Turner, Christopher M.

TITLE OF INVENTION: PROSTATE CANCER MARKERS

FILE REFERENCE: PA-0036 US

CURRENT APPLICATION NUMBER: US/09/919,172

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/222,469

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PERL Program

SEQ ID NO 15

LENGTH: 4108

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incycle ID No. 6673545 3615080CB1

US-09-919-172-15

Query Match 82.2%; Score 14.8; DB 3; Length 4108;

Best Local Similarity 88.9%; Pred. No. 2.6e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGACCTAGAGCAAG 18

Db 2065 CGATCCTAGATGCAAG 2082

RESULT 29

US-07-841-646-3
Sequence 3, Application US/07841646

Patent No. 5266683

GENERAL INFORMATION:

APPLICANT: OPPERMAN, HERMANN

APPLICANT: OZKAYNAK, ENGIN

APPLICANT: KUBERASAMPATH, THANGAVEL

APPLICANT: RUEGER, DAVID C.

APPLICANT: PANG, ROY H.L.

TITLE OF INVENTION: OSTEOGENIC DEVICES

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: TESTA, HURWITZ & THIBEAULT

STREET: 53 STATE STREET

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: U.S.A.

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/841,646

FILING DATE: 19920221

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 810,560

FILING DATE: 20-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 827,052

FILING DATE: 28-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 660,162

FILING DATE: 22-FEB-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 621,988

FILING DATE: 04-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 621,849

FILING DATE: 04-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 616,374

FILING DATE: 21-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 600,024

FILING DATE: 18-OCT-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 599,543

FILING DATE: 18-OCT-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 579,865

FILING DATE: 07-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 569,920

FILING DATE: 20-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 483,913

FILING DATE: 22-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 422,613

FILING DATE: 17-OCT-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 315,342

FILING DATE: 23-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 232,630

FILING DATE: 15-AUG-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 179,460

FILING DATE: 08-APR-1988

PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

NAME: PITCHER, EDWARD R.

REGISTRATION NUMBER: 27,829

REFERENCE/DOCKET NUMBER: CRP-001CP6

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/248-7000

TELEFAX: 617/248-7100

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 17410 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: homo sapiens

FEATURE:

NAME/KEY: exon

LOCATION: 3192..3730

OTHER INFORMATION: /label= EXON-1

OTHER INFORMATION: /note= "START CODON BEGINS AT POSITION 3313"

FEATURE:

NAME/KEY: misc feature

LOCATION: 10413..10414

OTHER INFORMATION: /label= GAP-1

OTHER INFORMATION: /note= "APPROXIMATELY BASES ARE ESTIMATED TO BE MISSING BETWEEN POSITIONS 10413 AND 10414 IN THIS SEQUENCE."

FEATURE:

NAME/KEY: exon

LOCATION: 10696..10891

OTHER INFORMATION: /label= EXON-2

OTHER INFORMATION: /label= GAP-2

OTHER INFORMATION: /note="APPROXIMATELY BASES ARE ESTIMATED TO
OTHER INFORMATION: BE MISSING BETWEEN POSITION 10960 AND 10961 IN
OTHER INFORMATION: THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 11059..11211
OTHER INFORMATION: /label= EXON-3
FEATURE:
NAME/KEY: misc feature
LOCATION: 11351..11352
OTHER INFORMATION: /label= GAP-3
OTHER INFORMATION: /note="APPROXIMATELY BASES ARE ESTIMATED TO
OTHER INFORMATION: BE MISSING BETWEEN POSITIONS 11351 AND 11352 IN
OTHER INFORMATION: THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 11420..11617
OTHER INFORMATION: /label= EXON-4
FEATURE:
NAME/KEY: misc feature
LOCATION: 11721..11722
OTHER INFORMATION: /label= GAP-4
OTHER INFORMATION: /note="APPROXIMATELY BASES ARE ESTIMATED TO
OTHER INFORMATION: BE MISSING BETWEEN POSITIONS 11721 AND 11722 IN
OTHER INFORMATION: THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 13354..13436
OTHER INFORMATION: /label= EXON-5
FEATURE:
NAME/KEY: exon
LOCATION: 15044..15160
OTHER INFORMATION: /label= EXON-6
FEATURE:
NAME/KEY: exon
LOCATION: 17245..17410
OTHER INFORMATION: /label= EXON-7
US-07-841-646-3

Query Match 82.2% Score 14.8; DB 2; Length 17410;
Best Local Similarity 88.9%; Pred. No. 38+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCGACCTAGAGCAAG 18
DB 14427 CAGACCTAGAGCAAG 14444

RESULT 30
US-08-147-023-3
Sequence 3, Application US/08147023
Patent No. 5468845
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMANN
APPLICANT: OKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H. L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/147,023
FILING DATE: 21-FEB-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: 3192..3730
OTHER INFORMATION: /label= EXON-1
OTHER INFORMATION: /note="START CODON BEGINS AT POSITION 3313"
FEATURE:
NAME/KEY: misc feature
LOCATION: 10413..10414
OTHER INFORMATION: /label= GAP-1

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OTHER INFORMATION: /note="APPROXIMATELY" BASES ARE ESTIMATED TO
OTHER INFORMATION: BE MISSING BETWEEN POSITIONS 10413 AND 10414 IN
OTHER INFORMATION: THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 10696..10891
OTHER INFORMATION: //label= EXON-2
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10960..10961
OTHER INFORMATION: //label= GAP-2
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US-08-147-023-3

Query Match      82.2%; Score 14.8; DB 2; Length 17410;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGAGCCTAGAGGCAAG 18
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Db      14427 CAGACCTAGAGGCAAG 14444
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Search completed: April 15, 2006, 20:30:30
Job time : 205 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 19:30:59 ; Search time 673 Seconds
(without alignments)
178.253 Million cell updates/sec

Title: US-10-727-358-5
Perfect score: 18
Sequence: 1 cggaccctcagagcaag 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 300 summaries

Database :

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1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002as.*
7: geneseqn2002bs.*
8: geneseqn2003as.*
9: geneseqn2003bs.*
10: geneseqn2003cs.*
11: geneseqn2003ds.*
12: geneseqn2004as.*
13: geneseqn2004bs.*
14: geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	18	12	ADG75398 Human kin
2	18	100.0	18	12	ADG75391 Human kin
3	18	100.0	18	14	AEA46548 Kinase su
4	18	100.0	18	14	AEA46538 Kinase su
5	18	100.0	18	14	AEA46561 Kinase su
6	18	100.0	120	14	AEA46534 Kinase su
7	18	100.0	121	14	AEA46557 Kinase su
8	18	100.0	2601	14	AEA46557 Human kin
9	18	100.0	4034	14	AEA46544 Mouse kin
10	18	100.0	4094	2	AAT72155 Mouse Ksr
11	18	100.0	4094	12	ADG75394 Mouse kin
12	18	88.9	16	14	AEA46541 Kinase su
13	15.4	85.6	376	6	ABL67488 Thyroid c
14	15.4	85.6	376	6	ABL69201 Prostata
15	15.4	85.6	388	10	ADP80786 Leukaemia
16	15.4	85.6	514	4	AAK86398 Human dig
17	15.4	85.6	514	5	AAK86398 Human enco
18	15.4	85.6	514	9	ADB32225 Human nov
19	15.4	85.6	986	10	ADP82177 Leukaemia

C 20	15.4	85.6	1797	12	ADQ24821	Adq24821 Human sof
C 21	15.4	85.6	9645	12	ADQ18079	Adq18079 Human sof
C 22	15.4	85.6	20001	14	ADZ59509	Adz59509 Secondary
C 23	15.4	85.6	22475	12	ADQ97998	Adq97998 Human can
C 24	15.4	85.6	191150	12	ADM69029	Adm69029 Human pla
C 25	15	83.3	50	6	ABZ07598	Abz07598 Human leu
C 26	15	83.3	50	12	ADP10220	Adp10220 50-mer o1
C 27	15	83.3	51	4	AAI76987	Aai76987 Human s11
C 28	15	83.3	51	4	AAI76986	Aai76986 Human s11
C 29	15	83.3	75	6	ABQ95689	Abq95689 Tumour su
C 30	15	83.3	163	3	AAAC24825	Aac24825 Human sec
C 31	15	83.3	230	12	ADQ40865	Adq40865 Human CDN
C 32	15	83.3	345	6	ABL38407	AbL38407 Human col
C 33	15	83.3	412	9	ACH49943	Ach49943 Human leu
C 34	15	83.3	444	6	ABK36157	Abk36157 CDNA sequ
C 35	15	83.3	461	13	ACF83765	Acf83765 Human SIR
C 36	15	83.3	478	9	ACH29337	Ach29337 Human adu
C 37	15	83.3	495	12	ADQ00107	Adq00107 Human adu
C 38	15	83.3	495	12	ADN98538	Adn98538 Novel hum
C 39	15	83.3	554	4	AAK35449	Aak35449 Human car
C 40	15	83.3	554	10	ADB45528	AdB45528 Human car
C 41	15	83.3	554	13	ADJ06946	Adj06946 Human car
C 42	15	83.3	627	10	ADB47513	AdB47513 Human CDN
C 43	15	83.3	645	9	AAK57225	Aak57225 Human CGD
C 44	15	83.3	764	12	ADP10552	Adp10552 Reference
C 45	15	83.3	765	3	AAA59670	AaA59670 DNA encod
C 46	15	83.3	779	6	ABK36158	Abk36158 CDNA sequ
C 47	15	83.3	782	5	AAH68582	Aah68582 Human pro
C 48	15	83.3	783	3	AAA14823	AaA14823 DNA encod
C 49	15	83.3	784	6	ABA98935	AbA98935 Human TGF
C 50	15	83.3	803	14	AEA20476	Aea20476 Novel hum
C 51	15	83.3	825	14	AEA19346	Aea19346 Novel hum
C 52	15	83.3	868	6	ABE70502	AbE70502 Human bon
C 53	15	83.3	2278	11	ADM01377	Adm01377 Human CDN
C 54	15	83.3	2399	11	ADI31182	Adi31182 Human CDN
C 55	15	83.3	2399	13	ADS83249	AdS83249 Human lym
C 56	15	83.3	5760	4	ABL17686	AbL17686 Drosophil
C 57	15	83.3	44749	11	ACN44034	Acn44034 Human gen
C 58	15	83.3	110000	13	ABD32627	Abd32627 Continuation (3 of
C 59	15	83.3	122937	13	ABD33516	Abd33516 Human can
C 60	14.8	82.2	399	3	AAA82091	AaA82091 N. mening
C 61	14.8	82.2	1115	13	ADK64023	AdK64023 Plant ful
C 62	14.8	82.2	1149	9	ADA48879	Ada48879 Banana ge
C 63	14.8	82.2	1149	11	ACL31234	AcL31234 Rice abio
C 64	14.8	82.2	2005	13	ADR62571	AdR62571 Cotton CD
C 65	14.8	82.2	2044	6	ABK35181	AbK35181 Human CDN
C 66	14.8	82.2	2204	3	AAA53720	AaA53720 Human pho
C 67	14.8	82.2	2605	8	ACG77209	AcG77209 Thernus s
C 68	14.8	82.2	2661	9	ADA15655	Ada15655 Human kin
C 69	14.8	82.2	2703	9	ADA15657	Ada15657 Human kin
C 70	14.8	82.2	2846	2	AAT72156	Aat72156 Human Ksr
C 71	14.8	82.2	2870	4	ABL15818	AbL15818 Drosophil
C 72	14.8	82.2	3006	4	ABL16372	AbL16372 Drosophil
C 73	14.8	82.2	3011	12	ADQ36007	AdQ36007 Novel mou
C 74	14.8	82.2	3342	13	ADR08122	AdR08122 Full leng
C 75	14.8	82.2	3357	12	ADQ64764	AdQ64764 Novel hum
C 76	14.8	82.2	3469	3	AAK3728	Aak3728 Human lam
C 77	14.8	82.2	3511	3	AAK3726	Aak3726 Human lam
C 78	14.8	82.2	3516	2	AAV29044	Aav29044 Open read
C 79	14.8	82.2	3519	14	ADV67470	Adv67470 Nucleotid
C 80	14.8	82.2	3585	3	AAK3727	Aak3727 Human lam
C 81	14.8	82.2	3621	3	AAK3725	Aak3725 Human lam
C 82	14.8	82.2	3759	3	AAK3724	Aak3724 Human lam
C 83	14.8	82.2	3810	8	ACC72088	Acc72088 Human NOV
C 84	14.8	82.2	3930	3	AAO89871	Aao89871 Laminin B
C 85	14.8	82.2	3930	3	AAK3723	Aak3723 Human lam
C 86	14.8	82.2	3971	6	AAK28066	Aak28066 LamininB
C 87	14.8	82.2	3971	8	ABX76133	Abx76133 lung can
C 88	14.8	82.2	3971	8	ABX76390	Abx76390 lung can
C 89	14.8	82.2	3971	8	ACC72087	Acc72087 Human NOV
C 90	14.8	82.2	3971	10	ADC01884	Adc01884 Human DNA
C 91	14.8	82.2	3971	11	ADN39001	Adn39001 Cancer/an
C 92	14.8	82.2	3971	13	ACN37576	Acn37576 Tumour-ab

93	14.8	82.2	4108	6	ABSG62737	AbSG62737	Prostate	C 166	14.4	80.0	103747	6	ABG88139	AbG88139	Human ost
94	14.8	82.2	4108	8	ABX77550	AbX77550	Different	C 167	14.4	80.0	110000	12	ADN46845_17	ADN46845_17	Continuation (18 o
95	14.8	82.2	4108	8	ABX63559	AbX63559	Human CDN	C 168	14.4	80.0	110000	12	ADN47591_03	ADN47591_03	Continuation (4 of
96	14.8	82.2	4108	14	ADV85764	ADV85764	Human CDN	C 169	14.4	80.0	110000	12	ADN46123_17	ADN46123_17	Continuation (18 o
97	14.8	82.2	4667	2	AAV29043	AAV29043	Human pro	C 170	14.4	80.0	110000	12	ADN47209_03	ADN47209_03	Continuation (4 of
98	14.8	82.2	4816	10	ADBS4538	ADBS4538	Rat gene	C 171	14.4	80.0	110000	12	ADN46464_17	ADN46464_17	Continuation (18 o
99	14.8	82.2	4816	10	ADBS4542	ADBS4542	Rat gene	C 172	14.4	80.0	110000	12	ADN47960_03	ADN47960_03	Continuation (4 of
100	14.8	82.2	5913	12	ADJ96596	ADJ96596	Human tyr	C 173	14.4	80.0	110000	14	ABE42401_21	ABE42401_21	Continuation (22 o
101	14.8	82.2	17350	2	AAQ72708	AAQ72708	hOP1 huma	C 174	14.4	80.0	115218	8	ACA64845	ACA64845	Human HNR
102	14.8	82.2	17410	2	AAO53142	AAO53142	Sequence	C 175	14.4	80.0	116704	11	ACN44818	ACN44818	Human gen
103	14.8	82.2	17410	2	AAAT18381	AAAT18381	hOP-1 gen	C 176	14.4	80.0	127767	13	ABD33584	ABD33584	Murine ca
104	14.8	82.2	17410	2	AAV15205	AAV15205	Human ost	C 177	14.4	80.0	127767	13	ADP67023	ADP67023	Mouse can
105	14.8	82.2	17410	2	AAV00230	AAV00230	Human ost	C 178	14.4	80.0	127767	14	ADZ13356	ADZ13356	Murine ca
106	14.8	82.2	17410	2	AAZ27575	AAZ27575	Human ost	C 179	14.4	80.0	134499	3	AAF22286	AAF22286	BAC conta
107	14.8	82.2	17410	10	ADJ62678	ADJ62678	Human ost	C 180	14.4	80.0	142976	13	ABD32612	ABD32612	Human can
108	14.8	82.2	17410	12	ADBS2749	ADBS2749	Human ost	C 181	14.4	80.0	150201	14	ADZ13203	ADZ13203	Human can
109	14.8	82.2	17410	12	ADM80487	ADM80487	Human ost	C 182	14.4	80.0	329019	13	ABD32707	ABD32707	Human can
110	14.8	82.2	17410	13	ADDO3609	ADDO3609	Genomic D	C 183	14.4	77.8	247	13	AAO14378	AAO14378	FP22x4 pr
111	14.8	82.2	17415	2	AAV11639	AAV11639	Human ost	C 184	14.4	77.8	315	6	ABQ90769	ABQ90769	M. capsul
112	14.8	82.2	17415	2	AAV80733	AAV80733	Human ost	C 185	14.4	77.8	385	6	ABK62977	ABK62977	Rat seque
113	14.8	82.2	17415	2	AAA59897	AAA59897	Human DNA	C 186	14.4	77.8	585	10	ADB57048	ADB57048	Toxicity-
114	14.8	82.2	97700	10	ADL13678	ADL13678	Osteoarthritis	C 187	14.4	77.8	585	12	ADP72219	ADP72219	Renal tox
115	14.8	82.2	101786	3	AAE22293	AAE22293	BAC conta	C 188	14.4	77.8	616	13	AAFO9798	AAFO9798	Fusarium
116	14.8	82.2	110000	12	ADOF78173_3	ADOF78173_3	Continuation (4 of	C 189	14.4	77.8	616	13	ADU53839	ADU53839	Fusarium
117	14.8	82.2	117750	13	ABD32653	ABD32653	Human can	C 190	14.4	77.8	616	14	ADZ91882	ADZ91882	Fusarium
118	14.4	80.0	201	13	ADS40630	ADS40630	Human aut	C 191	14.4	77.8	1317	4	ABL13055	ABL13055	Novel hum
119	14.4	80.0	364	3	AAAC22364	AAAC22364	Human sec	C 192	14.4	77.8	2298	12	ADQ63262	ADQ63262	DNA encod
120	14.4	80.0	367	8	ABE256573	ABE256573	Aspergill	C 193	14.4	77.8	2445	12	ADQ57280	ADQ57280	EGFR geno
121	14.4	80.0	380	13	ADRF4186	ADRF4186	Bovine ES	C 194	14.4	77.8	6274	10	ADBS3967	ADBS3967	Continuation (4 of
122	14.4	80.0	419	5	AAE29846	AAE29846	Human lun	C 195	14.4	77.8	8979	4	ABL13054	ABL13054	Continuation (4 of
123	14.4	80.0	475	5	AAE29846	AAE29846	Human lun	C 196	14.4	77.8	110000	3	AAF22305_03	AAF22305_03	Continuation (4 of
124	14.4	80.0	475	6	ABL64293	ABL64293	Stomach c	C 197	14.4	77.8	110000	6	ABBS5320_3	ABBS5320_3	Continuation (4 of
125	14.4	80.0	479	6	ABL64293	ABL64293	Stomach c	C 198	14.4	77.8	110000	6	ABBS5320_0	ABBS5320_0	Continuation (4 of
126	14.4	80.0	483	4	AAK48139	AAK48139	Zea maye	C 199	14.4	77.8	110000	12	ADQ59398	ADQ59398	Human can
127	14.4	80.0	498	4	AAK79223	AAK79223	Human imm	C 200	14.4	77.8	110000	14	ADZ13665_0	ADZ13665_0	Human can
128	14.4	80.0	552	6	ABK90877	ABK90877	CDNA enco	C 201	14.4	77.8	189013	8	ACF62741	ACF62741	Cancer ba
129	14.4	80.0	564	8	ABE257962	ABE257962	Human sec	C 202	14.4	77.8	189013	8	ADB20856	ADB20856	MRP1 base
130	14.4	80.0	581	8	ACD20381	ACD20381	DNA encod	C 203	14.4	77.8	189013	10	ADB87945	ADB87945	Human UGT
131	14.4	80.0	592	12	ACH73816	ACH73816	Human gen	C 204	14.4	77.8	189013	10	ADB86928	ADB86928	Human MDR
132	14.4	80.0	621	4	ABL25863	ABL25863	Drosophill	C 205	14.4	77.8	189013	10	ADB92119	ADB92119	Human MDR
133	14.4	80.0	636	5	ABV50466	ABV50466	Human pro	C 206	14.4	77.8	197496	6	ABN85584	ABN85584	Human EGF
134	14.4	80.0	658	3	AAAC57768	AAAC57768	Arachidon	C 207	14.4	77.8	209083	13	ABD32854	ABD32854	Human can
135	14.4	80.0	887	13	ADSI10299	ADSI10299	Human the	C 208	14.4	77.8	251364	13	ADV35003	ADV35003	Murine can
136	14.4	80.0	939	3	AAAC57769	AAAC57769	Arachidon	C 209	14.4	77.8	251364	13	ADV34965	ADV34965	Murine CD
137	14.4	80.0	1022	2	AAZ11769	AAZ11769	Maize elo	C 210	14.4	77.8	251364	13	ADV34982	ADV34982	Murine CD
138	14.4	80.0	2136	13	ADM54721	ADM54721	Plant ful	C 211	14.4	77.8	341511	5	ABBS5200	ABBS5200	Genomic D
139	14.4	80.0	2195	12	ABT23862	ABT23862	Murine ad	C 212	14.4	77.8	349980	5	AAH41224	AAH41224	Pyrococcu
140	14.4	80.0	2621	4	ABT23862	ABT23862	Drosophill	C 213	13.8	76.7	20	2	AAK96257	AAK96257	PCR prime
141	14.4	80.0	2754	3	AAAC45843	AAAC45843	Arabidops	C 214	13.8	76.7	25	9	ACT102856	ACT102856	Human mic
142	14.4	80.0	2754	6	ABZ13981	ABZ13981	Arabidops	C 215	13.8	76.7	41	2	AAV50875	AAV50875	Maize pol
143	14.4	80.0	2754	8	ADA68022	ADA68022	Arabidops	C 216	13.8	76.7	50	4	AAI78755	AAI78755	Human sil
144	14.4	80.0	2754	12	ADN72372	ADN72372	Thale cre	C 217	13.8	76.7	51	4	AAI78754	AAI78754	Human sil
145	14.4	80.0	3153	10	ADB62173	ADB62173	Human CDN	C 218	13.8	76.7	121	12	ADK92695	ADK92695	SNP target
146	14.4	80.0	4857	4	AAK80786	AAK80786	Human imm	C 219	13.8	76.7	135	12	ADK93249	ADK93249	Polynucle
147	14.4	80.0	5122	4	AAK80784	AAK80784	Human imm	C 220	13.8	76.7	147	14	ADV04873	ADV04873	Yersinia
148	14.4	80.0	5122	4	AAK80787	AAK80787	Human imm	C 221	13.8	76.7	151	14	AEBS85384	AEBS85384	Human pho
149	14.4	80.0	5122	4	AAK80785	AAK80785	Human imm	C 222	13.8	76.7	165	6	ABK79320	ABK79320	Bacillus
150	14.4	80.0	6951	10	ADG32852	ADG32852	Human DNA	C 223	13.8	76.7	215	2	AAV69787	AAV69787	EST clone
151	14.4	80.0	6995	10	ADFS926	ADFS926	Human con	C 224	13.8	76.7	235	3	AAAC13109	AAAC13109	Human sec
152	14.4	80.0	7036	8	ABE257963	ABE257963	Human sec	C 225	13.8	76.7	262	4	AD140326	AD140326	Human pur
153	14.4	80.0	7376	4	AAK68043	AAK68043	Human imm	C 226	13.8	76.7	262	4	AAK59014	AAK59014	Human imm
154	14.4	80.0	7888	13	ADR83507	ADR83507	Human mul	C 227	13.8	76.7	266	4	AAK74307	AAK74307	Human imm
155	14.4	80.0	8323	2	AAO58700	AAO58700	LTR clone	C 228	13.8	76.7	266	4	AAK74305	AAK74305	Human imm
156	14.4	80.0	8323	2	AAO81042	AAO81042	Friend mu	C 229	13.8	76.7	266	4	AAK74306	AAK74306	Human imm
157	14.4	80.0	8323	2	AAAT80058	AAAT80058	LTR clone	C 230	13.8	76.7	302	2	AAI31590	AAI31590	Probe (BL
158	14.4	80.0	8323	2	AAZ07063	AAZ07063	Friend ec	C 231	13.8	76.7	304	4	AAK67036	AAK67036	Human imm
159	14.4	80.0	10367	2	AAQ58701	AAQ58701	PLRB332.	C 232	13.8	76.7	304	4	AAK67033	AAK67033	Human imm
160	14.4	80.0	10367	2	AAAT80057	AAAT80057	Sequence	C 233	13.8	76.7	314	4	AAK72213	AAK72213	DNA encod
161	14.4	80.0	10367	2	AAZ07067	AAZ07067	Glycocept	C 234	13.8	76.7	325	2	AAQ61199	AAQ61199	Human bra
162	14.4	80.0	16443	2	AAV83942	AAV83942	Bacterial	C 235	13.8	76.7	327	4	AAK61679	AAK61679	Human imm
163	14.4	80.0	19986	13	ADBS3481	ADBS3481	Human aut	C 236	13.8	76.7	337	12	ADQ19132	ADQ19132	Human sof
164	14.4	80.0	21429	4	AAE57362	AAE57362	Murine Cd	C 237	13.8	76.7	343	4	AAK55228	AAK55228	Human imm
165	14.4	80.0	71953	11	ACN44552	ACN44552	Mouse gen	C 238	13.8	76.7	353	4	AAI14002	AAI14002	Probe #39

C 239	13.8	76.7	353	4	ABA55727	Human foe
C 240	13.8	76.7	353	4	AAI35382	Probe #40
C 241	13.8	76.7	353	4	ABA45235	Human bre
C 242	13.8	76.7	353	4	ABA25410	Probe #38
C 243	13.8	76.7	353	4	AAK29426	Human bon
C 244	13.8	76.7	353	4	AAK03949	Human bra
C 245	13.8	76.7	353	4	ABS29053	Human liv
C 246	13.8	76.7	353	5	AAI03861	Probe #38
C 247	13.8	76.7	353	6	ABS03981	Human gen
C 248	13.8	76.7	357	11	ACI33699	Rice ablo
C 249	13.8	76.7	369	6	ABK72169	Lymphona
C 250	13.8	76.7	369	12	ADM79223	Mouse Lym
C 251	13.8	76.7	371	4	ABA75195	Human foe
C 252	13.8	76.7	371	4	AAI55744	Probe #24
C 253	13.8	76.7	371	4	AAK49827	Human bon
C 254	13.8	76.7	371	4	AAK23730	Human bra
C 255	13.8	76.7	371	6	ABS23331	Human gen
C 256	13.8	76.7	374	4	ABA73972	Human foe
C 257	13.8	76.7	374	4	AAI54421	Probe #23
C 258	13.8	76.7	374	4	AAK46592	Human bon
C 259	13.8	76.7	374	4	AAK22425	Human bra
C 260	13.8	76.7	374	4	ABS48277	Human liv
C 261	13.8	76.7	374	6	ABS22353	Human gen
C 262	13.8	76.7	375	6	ABN76814	Human ORF
C 263	13.8	76.7	378	4	AAI23005	Probe #12
C 264	13.8	76.7	378	4	ABA68096	Human foe
C 265	13.8	76.7	378	4	AAI48305	Probe #16
C 266	13.8	76.7	378	4	ABA50162	Human bre
C 267	13.8	76.7	378	4	ABA35125	Probe #13
C 268	13.8	76.7	378	4	AAK42235	Human bon
C 269	13.8	76.7	378	4	AAK16483	Human bra
C 270	13.8	76.7	378	4	ABA41841	Human liv
C 271	13.8	76.7	378	5	AAI08668	Probe #86
C 272	13.8	76.7	378	6	ABS16285	Human gen
C 273	13.8	76.7	383	4	AAI23099	Probe #13
C 274	13.8	76.7	383	4	AAI21743	Probe #11
C 275	13.8	76.7	383	4	AAI21300	Probe #11
C 276	13.8	76.7	383	4	ABA68190	Human foe
C 277	13.8	76.7	383	4	ABA66383	Human foe
C 278	13.8	76.7	383	4	ABA66819	Human foe
C 279	13.8	76.7	383	4	AAI47027	Probe #15
C 280	13.8	76.7	383	4	AAI46576	Probe #15
C 281	13.8	76.7	383	4	AAI48401	Probe #17
C 282	13.8	76.7	383	4	ABA48900	Human bre
C 283	13.8	76.7	383	4	ABA48478	Human bre
C 284	13.8	76.7	383	4	ABA50244	Human bre
C 285	13.8	76.7	383	4	ABA50244	Human bre
C 286	13.8	76.7	383	4	ABA33444	Probe #11
C 287	13.8	76.7	383	4	ABA33882	Probe #12
C 288	13.8	76.7	383	4	AAK42320	Human bon
C 289	13.8	76.7	383	4	AAK40539	Human bon
C 290	13.8	76.7	383	4	AAK40972	Human bon
C 291	13.8	76.7	383	4	AAI88464	Human pol
C 292	13.8	76.7	383	4	AAI52448	Human bra
C 293	13.8	76.7	383	4	AAK14798	Human bra
C 294	13.8	76.7	383	4	AAK16565	Human bra
C 295	13.8	76.7	383	4	ABA40102	Human liv
C 296	13.8	76.7	383	4	ABA41936	Human liv
C 297	13.8	76.7	383	4	ABA40556	Human liv
C 298	13.8	76.7	383	5	AAI07428	Probe #74
C 299	13.8	76.7	383	5	AAI07004	Probe #69
C 300	13.8	76.7	383	5	AAI08746	Probe #87

ALIGNMENTS

RESULT 1
ADG75398 standard; DNA; 18 BP.
XX
AC
XX

DT 11-MAR-2004 (first entry)
XX Human kinase suppressor of Ras (KSR)-specific oligonucleotide.
DE
XX antisense oligonucleotide; kinase suppressor of Ras; KSR; cancer;
KW pancreatic cancer; lung cancer; skin cancer; urinary tract cancer;
KW bladder cancer; liver cancer; thyroid cancer; colon cancer;
KW intestinal cancer; breast cancer; ovarian cancer; stomach cancer;
KW head cancer; neck cancer; esophageal cancer; prostate cancer; leukemia;
KW lymphoma; neuroblastoma; ss; human.
XX
OS Homo sapiens.
XX
XX W02003101386-A2.
XX
XX 11-DEC-2003.
XX
XX 29-MAY-2003; 2003WO-US016961.
XX
XX 30-MAY-2002; 2002US-0384228P.
XX
XX 03-APR-2003; 2003US-0460023P.
XX
XX (SLOK) SLOAN KETTERING INST CANCER RES.
XX
XX Kolesnick RM, Xing HR;
XX
XX WPI; 2004-053335/05.
XX
XX New antisense oligonucleotides complementary to a region of kinase
PT suppressor of Ras (KSR) RNA which inhibit KSR expression, useful for
PT treating or inhibiting progression of cancer, e.g. pancreatic, lung,
PT skin, or bladder cancer.
XX
XX Example 2; SEQ ID NO 15; 120bp; English.
XX
XX The invention comprises antisense oligonucleotides which are designed to
CC inhibit the expression of the kinase suppressor of Ras (KSR) gene. The
CC antisense oligonucleotides of the invention are useful for treating or
CC inhibiting the progression of cancer, such as: pancreatic cancer, lung
CC cancer, skin cancer, urinary tract cancer, bladder cancer, liver cancer,
CC thyroid cancer, colon cancer, intestinal cancer, breast cancer, ovarian
CC cancer, stomach cancer, head and neck cancer, esophageal cancer,
CC prostate cancer, leukemia, lymphoma, and neuroblastoma. The present DNA
CC sequence represents a human KSR-specific oligonucleotide that was used in
CC an example of the invention.
XX
SO Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGACCTTAGGCAAG 18
DB 1 CGGACCTTAGGCAAG 18
RESULT 2
ADG75391/C
ID ADG75391 standard; DNA; 18 BP.
XX
AC
XX
XX 11-MAR-2004 (first entry)
DE Human kinase suppressor of Ras (KSR) antisense oligonucleotide #3.
XX
XX antisense oligonucleotide; kinase suppressor of Ras; KSR; cancer;
KW pancreatic cancer; lung cancer; skin cancer; urinary tract cancer;
KW bladder cancer; liver cancer; thyroid cancer; colon cancer;
KW intestinal cancer; breast cancer; ovarian cancer; stomach cancer;
KW head cancer; neck cancer; esophageal cancer; prostate cancer; leukemia;
KW lymphoma; neuroblastoma; ss; human.

XX OS Homo sapiens.
 XX PN WO2003101386-A2.
 XX PD 11-DEC-2003.
 XX PF 29-MAY-2003; 2003WO-US016961.
 XX PR 30-MAY-2002; 2002US-0384228P.
 XX PR 03-APR-2003; 2003US-0460023P.
 XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX PI Kolesnick RN, Xing HR;
 XX DR WPI; 2004-053335/05.
 XX PS New antisense oligonucleotides complementary to a region of kinase
 PT suppressor of Ras (KSR) RNA which inhibit KSR expression, useful for
 PT treating or inhibiting progression of cancer, e.g. pancreatic, lung,
 PT skin, or bladder cancer.
 XX PS Claim 8; SEQ ID NO 8; 120pp; English.
 XX CC The invention comprises antisense oligonucleotides which are designed to
 CC inhibit the expression of the kinase suppressor of Ras (KSR) gene. The
 CC antisense oligonucleotides of the invention are useful for treating or
 CC inhibiting the progression of cancer, such as: pancreatic cancer, lung
 CC cancer, skin cancer, urinary tract cancer, bladder cancer, liver cancer,
 CC thyroid cancer, colon cancer, intestinal cancer, breast cancer, ovarian
 CC cancer, stomach cancer, head and neck cancer, esophageal cancer,
 CC prostate cancer, leukemia, lymphoma, and neuroblastoma. The present DNA
 CC sequence represents a human KSR-specific antisense oligonucleotide of the
 CC invention.
 XX SQ Sequence 18 BP; 1 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 XX Query Match 100.0%; Score 18; DB 12; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 21;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CGACCTTAGAGCAAG 18
 DB 18 CGACCTTAGAGCAAG 1
 RESULT 3
 AEA46548
 ID AEA46548 standard; DNA; 18 BP.
 XX AEA46548;
 XX 25-AUG-2005 (first entry)
 XX Kinase suppressor of Ras (KSR) antisense oligonucleotide, SEQ ID NO:15.
 XX Kinase suppressor of Ras; KSR; cytosolic; neoplasm; pancreas tumor;
 XX liver tumor; skin tumor; thyroid tumor; lung tumor; urinary tract tumor;
 XX gastrointestinal disease; respiratory disease; genitourinary disease;
 XX endocrine disease; bladder tumor; colon tumor; intestine tumor;
 XX head & neck tumor; leukemia; hematological disease; lymphoma;
 XX immune disorder; esophagus tumor; breast tumor; stomach tumor;
 XX nervous system tumor; neurological disease; ovary tumor;
 XX gynecology and obstetrics; ss; angiogenesis disorder; antiangiogenic;
 XX cardiovascular disease; antisense oligonucleotide; antisense therapy;
 XX prostate tumor; andrology; cancer; hyperproliferation.
 XX Homo sapiens.
 XX Mus sp.
 XX Synthetic.
 XX WO2005056756-A2.

XX PD 23-JUN-2005.
 XX PF 03-DEC-2004; 2004WO-US040506.
 XX PR 03-DEC-2003; 2003US-00727358.
 XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX PI Kolesnick RN, Xing HR;
 XX DR WPI; 2005-445165/45.
 XX PS Example 2; SEQ ID NO 15; 186pp; English.
 XX CC The invention relates to an oligonucleotide (I) which is substantially
 CC complementary to a region of kinase suppressor of Ras (KSR) RNA, where
 CC the oligonucleotide inhibits the expression of KSR. Also included are the
 CC following: an oligonucleotide (II) which is substantially complementary
 CC to a translation initiation site, 5' untranslated region, coding region
 CC or 3' untranslated region of mRNA encoding mammalian KSR; an antisense
 CC oligonucleotide (III) comprising a sequence substantially complementary
 CC to the CA1 region of KSR; an antisense oligonucleotide (IV) comprising a
 CC sequence substantially complementary to nucleotides 124-243 of the coding
 CC sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion;
 CC an antisense oligonucleotide (V) comprising a sequence chosen from
 CC AEA46539, AEA46540 and AEA46541, and ; a recombinant DNA molecule (VI)
 CC comprising a nucleic acid sequence which encodes on transcription an
 CC antisense RNA complementary to mammalian KSR RNA or its portion; a cell
 CC (VII) transfected with (VI); an expression vector (VI) capable of
 CC expressing a nucleic acid which is substantially complementary to the
 CC coding sequence of KSR RNA, or its portion/fragment, where the
 CC oligonucleotide/nucleic acid inhibits the expression of KSR; an
 CC expression vector (V2) capable of expressing an oligonucleotide which is
 CC substantially complementary to the CA1 region of the coding sequence of
 CC KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the
 CC expression of KSR; a pharmaceutical composition (PCI) comprising (I) and
 CC a carrier or diluent; a composition (C1) comprising (I) and a carrier or
 CC diluent; a composition (C2) comprising one or more chemotherapeutic or
 CC radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA
 CC encoding mammalian KSR and which inhibits KSR expression; a composition
 CC (C3) comprising an expression vector and a carrier or diluent, where the
 CC expression vector is capable of expressing nucleic acid which is
 CC substantially complementary to the coding sequence of KSR RNA, or its
 CC portion/fragment, where the nucleic acid inhibits the expression of KSR;
 CC inhibiting (M1) the expression of mammalian KSR comprising contacting
 CC cells which express KSR with a nucleic acid which is complementary to a
 CC portion of the mRNA encoding KSR; treating or preventing (M2) a
 CC hyperproliferative condition associated with the expression of gf-Ras or
 CC heightened expression of Ras in a mammal comprising administering to the
 CC mammal a compound or agent which inhibits the expression of mammalian KSR
 CC protein; treating or preventing (M3) a hyperproliferative condition
 CC associated with the expression of gf-Ras or heightened expression of Ras
 CC in a mammal comprising expressing in the mammal or administering to the
 CC mammal therapeutically effective amount of a nucleic acid which is
 CC complementary to a portion of the mRNA encoding KSR; treating or
 CC inhibiting (M4) the progression of cancer in a mammal comprising
 CC administering to a mammal a compound or agent which inhibits the
 CC expression of mammalian KSR protein; inhibiting angiogenesis of tumor
 CC cells in a mammal, by administering to a mammal a compound or agent which
 CC inhibits the expression of mammalian KSR protein; inhibiting or reducing
 CC VEGF expression or activity in a mammal, by administering a compound or
 CC agent that inhibits the expression of mammalian KSR protein; stimulating
 CC angiogenesis in a mammal comprising administering to a mammal a
 CC therapeutically effective amount of a compound or agent which activates
 CC the expression of mammalian KSR protein or a vector expressing mammalian
 CC KSR; identifying compounds or agents which inhibit the expression of KSR,
 CC by incubating a cell expressing KSR in the presence and absence of a

CC candidate compound or agent, and detecting or measuring the expression of
CC KSR in the presence and absence of a candidate compound or agent, where a
CC decrease in the expression of KSR in the presence of the candidate
CC compound or agent versus in the absence of the candidate compound or
CC agent indicates that the compound or agent inhibits the expression of KSR
CC ; and a ribozyme that cleaves KSR mRNA. (I) is useful for inhibiting the
CC expression of mammalian KSR comprising contacting cells which express KSR
CC with (I), where expression of mammalian KSR is inhibited. (I) is useful
CC for conferring radiosensitivity to ionizing radiation in tumor cells in a
CC mammal. (I) is useful for inhibiting angiogenesis in a mammal. (I) is
CC useful for inhibiting or reducing VEGF expression or activity in a
CC mammal. The methods are useful for treating or preventing
CC hyperproliferative condition associated with expression of gf-Ras or
CC heightened expression of Ras in a mammal and for treating or inhibiting
CC the progression of cancer in a mammal. The cancer is chosen from
CC pancreatic cancer, lung cancer, skin cancer, urinary tract cancer,
CC bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal
CC cancer, leukemia, lymphoma, neuroblastoma, head and neck cancer, breast
CC cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate
CC cancer. The present sequence represents a KSR antisense oligonucleotide.
XX
SQ Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pired. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGGACCTAGAGCGCAAG 18
1 CGGACCTAGAGCGCAAG 18
Db 1 CGGACCTAGAGCGCAAG 18
RESULT 4
AEA46538
ID AEA46538 standard; DNA; 18 BP.
XX
XX AEA46538;
AC
XX
XX 25-AUG-2005 (first entry)
DE Kinase suppressor of Ras (KSR) antisense oligonucleotide, SEQ ID NO:5.
XX
XX Kinase suppressor of Ras; KSR; cytostatic; neoplasm; pancreas tumor;
KM liver tumor; skin tumor; thyroid tumor; lung tumor; urinary tract tumor;
KM gastrointestinal disease; respiratory disease; genitourinary disease;
KM endocrine disease; bladder tumor; colon tumor; intestine tumor;
KM head & neck tumor; leukemia; hematological disease; lymphoma;
KM immune disorder; esophagus tumor; breast tumor; stomach tumor;
KM nervous system tumor; neurological disease; ovary tumor;
KM gynecology and obstetrics; es; angiogenesis disorder; antiangiogenic;
KM cardiovascular disease; antisense oligonucleotide; antisense therapy;
KM prostate tumor; andrology; cancer; hyperproliferation.
XX
XX Homo sapiens.
OS Mus sp.
OS Synthetic.
OS
XX
XX MO2005056756-A2.
XX
XX 23-JUN-2005.
PD
XX
XX 03-DEC-2004; 2004MO-US040506.
PF
XX
XX 03-DEC-2003; 2003US-00727358.
PR
XX
XX (SLOK) SLOAN KETTERING INST CANCER RES.
XX
XX Kolesnick RN, Xing HR;
PI
XX
XX WPI; 2005-445165/45.
DR
XX
XX New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression,
PT useful for inhibiting expression of mammalian KSR and treating

PT hyperproliferative conditions such as lung cancer, skin cancer, and
PT ovarian cancer.
XX
XX Claim 7; SEQ ID NO 5; 186pp; English.
XX
XX The invention relates to an oligonucleotide (I) which is substantially
CC complementary to a region of kinase suppressor of Ras (KSR) RNA, where
CC the oligonucleotide inhibits the expression of KSR. Also included are the
CC following: an oligonucleotide (II) which is substantially complementary
CC to a translation initiation site, 5' untranslated region, coding region
CC or 3' untranslated region of mRNA encoding mammalian KSR; an antisense
CC oligonucleotide (III) comprising a sequence substantially complementary
CC to the CAl region of KSR; an antisense oligonucleotide (IV) comprising a
CC sequence substantially complementary to nucleotides 124-243 of the coding
CC sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion;
CC an antisense oligonucleotide (V) comprising a sequence chosen from
CC AEA46539, AEA46540 and AEA46541, and; a recombinant DNA molecule (VI)
CC comprising a nucleic acid sequence which encodes or transcribes an
CC antisense RNA complementary to mammalian KSR RNA or its portion; a cell
CC (VII) transfected with (VI); an expression vector (VI) capable of
CC expressing a nucleic acid which is substantially complementary to the
CC coding sequence of KSR RNA, or its portion/fragment, where the
CC oligonucleotide/nucleic acid inhibits the expression of KSR; an
CC expression vector (V2) capable of expressing an oligonucleotide which is
CC substantially complementary to the CAl region of the coding sequence of
CC KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the
CC expression of KSR; a pharmaceutical composition (PC1) comprising (I) and
CC a carrier or diluent; a composition (C1) comprising (I) and a carrier or
CC diluent; a composition (C2) comprising one or more chemotherapeutic or
CC radiotherapeutic agent and an oligonucleotide which is targeted to a RNA
CC encoding mammalian KSR and which inhibits KSR expression; a composition
CC (C3) comprising an expression vector and a carrier or diluent, where the
CC expression vector is capable of expressing nucleic acid which is
CC substantially complementary to the coding sequence of KSR RNA, or its
CC portion/fragment, where the nucleic acid inhibits the expression of KSR;
CC inhibiting (M1) the expression of mammalian KSR comprising contacting
CC cells which express KSR with a nucleic acid which is complementary to a
CC portion of the mRNA encoding KSR; treating or preventing (M2) a
CC hyperproliferative condition associated with the expression of gf-Ras or
CC heightened expression of Ras in a mammal comprising administering to the
CC mammal a compound or agent which inhibits the expression of mammalian KSR
CC protein; treating or preventing (M3) a hyperproliferative condition
CC associated with the expression of gf-Ras or heightened expression of Ras
CC in a mammal comprising expressing in the mammal or administering to the
CC mammal therapeutically effective amount of a nucleic acid which is
CC complementary to a portion of the mRNA encoding KSR; treating or
CC inhibiting (M4) the progression of cancer in a mammal comprising
CC administering to a mammal a compound or agent which inhibits the
CC expression of mammalian KSR protein; inhibiting angiogenesis of tumor
CC cells in a mammal, by administering to a mammal a compound or agent which
CC inhibits the expression of mammalian KSR protein; inhibiting or reducing
CC VEGF expression or activity in a mammal, by administering a compound or
CC agent that inhibits the expression of mammalian KSR protein; stimulating
CC angiogenesis in a mammal comprising administering to a mammal a
CC therapeutically effective amount of a compound or agent which activates
CC the expression of mammalian KSR protein or a vector expressing mammalian
CC KSR; identifying compounds or agents which inhibit the expression of KSR,
CC by incubating a cell expressing KSR in the presence and absence of a
CC candidate compound or agent, and detecting or measuring the expression of
CC KSR in the presence and absence of a candidate compound or agent, where a
CC decrease in the expression of KSR in the presence of the candidate
CC compound or agent versus in the absence of the candidate compound or
CC agent indicates that the compound or agent inhibits the expression of KSR
CC ; and a ribozyme that cleaves KSR mRNA. (I) is useful for inhibiting the
CC expression of mammalian KSR comprising contacting cells which express KSR
CC with (I), where expression of mammalian KSR is inhibited. (I) is useful
CC for conferring radiosensitivity to ionizing radiation in tumor cells in a
CC mammal. (I) is useful for inhibiting angiogenesis in a mammal. (I) is
CC useful for inhibiting or reducing VEGF expression or activity in a
CC mammal. The methods are useful for treating or preventing
CC hyperproliferative condition associated with expression of gf-Ras or
CC heightened expression of Ras in a mammal and for treating or inhibiting
CC the progression of cancer in a mammal. The cancer is chosen from

CC pancreatic cancer, lung cancer, skin cancer, urinary tract cancer,
CC bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal
CC cancer, leukemia, lymphoma, neuroblastoma, head and neck cancer, breast
CC cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate
CC cancer. The present sequence represents a KSR antisense oligonucleotide.
XX
SQ Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGACCTAGAGGCAAG 18
Db 1 CGGACCTAGAGGCAAG 18
RESULT 5
AEA46561/C
ID AEA46561 standard; DNA; 18 BP.
XX
AC AEA46561;
XX
DT 25-AUG-2005 (first entry)
XX
XX Kinase suppressor of Ras (KSR) antisense oligonucleotide, SEQ ID NO:28.
XX
KM Kinase suppressor of Ras; KSR; cytosolic; neoplasm; pancreas tumor;
KM liver tumor; skin tumor; thyroid tumor; lung tumor; urinary tract tumor;
KM gastrointestinal disease; respiratory disease; genitourinary disease;
KM endocrine disease; bladder tumor; colon tumor; intestine tumor;
KM head & neck tumor; leukemia; hematological disease; lymphoma;
KM immune disorder; esophagus tumor; breast tumor; stomach tumor;
KM nervous system tumor; neurological disease; ovary tumor;
KM gynecology and obstetrics; ss; angiogenesis disorder; angiogenic;
KM cardiovascular disease; antisense oligonucleotide; antisense therapy;
KM prostate tumor; andrology; cancer; hyperproliferation.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
PN WO2005056756-A2.
XX
PD 23-JUN-2005.
XX
XX 03-DEC-2004; 2004WO-US040506.
XX
XX 03-DEC-2003; 2003US-00727358.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI Kolesnick RN, Xing HR;
XX
DR WPI; 2005-445165/45.
XX
PT New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression,
PT useful for inhibiting expression of mammalian KSR and treating
PT hyperproliferative conditions such as lung cancer, skin cancer, and
PT ovarian cancer.
XX
PS Claim 8; SEQ ID NO 28; 186pp; English.
XX
XX The invention relates to an oligonucleotide (I) which is substantially
XX complementary to a region of kinase suppressor of Ras (KSR) RNA, where
XX the oligonucleotide inhibits the expression of KSR. Also included are the
XX following: an oligonucleotide (II) which is substantially complementary
XX to a translation initiation site, 5' untranslated region, coding region
XX or 3' untranslated region of mRNA encoding mammalian KSR; an antisense
XX oligonucleotide (III) comprising a sequence substantially complementary
XX to the 3' region of KSR; an antisense oligonucleotide (IV) comprising a
XX sequence substantially complementary to nucleotides 124-243 of the coding
XX sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion;

CC an antisense oligonucleotide (V) comprising a sequence chosen from
CC AEA46539, AEA46540 and AEA46541, and ; a recombinant DNA molecule (VI)
CC comprising a nucleic acid sequence which encodes or transcribes an
CC antisense RNA complementary to mammalian KSR RNA or its portion; a cell
CC (VII) transfected with (VI); an expression vector (VI) capable of
CC expressing a nucleic acid which is substantially complementary to the
CC coding sequence of KSR RNA, or its portion/fragment, where the
CC oligonucleotide/nucleic acid inhibits the expression of KSR; an
CC expression vector (V2) capable of expressing an oligonucleotide which is
CC substantially complementary to the 3' region of the coding sequence of
CC KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the
CC expression of KSR; a pharmaceutical composition (PC1) comprising (I) and
CC a carrier or diluent; a composition (C1) comprising (I) and a carrier or
CC diluent; a composition (C2) comprising one or more chemotherapeutic or
CC radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA
CC encoding mammalian KSR and which inhibits KSR expression; a composition
CC (C3) comprising an expression vector and a carrier or diluent, where the
CC expression vector is capable of expressing nucleic acid which is
CC substantially complementary to the coding sequence of KSR RNA, or its
CC portion/fragment, where the nucleic acid inhibits the expression of KSR;
CC inhibiting (M1) the expression of mammalian KSR comprising contacting
CC cells which express KSR with a nucleic acid which is complementary to a
CC portion of the mRNA encoding KSR; treating or preventing (M2) a
CC hyperproliferative condition associated with the expression of gf-Ras or
CC heightened expression of Ras in a mammal comprising administering to the
CC mammal a compound or agent which inhibits the expression of mammalian KSR
CC protein; treating or preventing (M3) a hyperproliferative condition
CC associated with the expression of gf-Ras or heightened expression of Ras
CC in a mammal comprising expressing in the mammal or administering to the
CC mammal therapeutically effective amount of a nucleic acid which is
CC complementary to a portion of the mRNA encoding KSR; treating or
CC inhibiting (M4) the progression of cancer in a mammal comprising
CC administering to a mammal a compound or agent which inhibits the
CC expression of mammalian KSR protein; inhibiting angiogenesis of tumor
CC cells in a mammal, by administering to a mammal a compound or agent which
CC inhibits the expression of mammalian KSR protein; inhibiting or reducing
CC VEGF expression or activity in a mammal, by administering a compound or
CC agent that inhibits the expression of mammalian KSR protein; stimulating
CC angiogenesis in a mammal comprising administering to a mammal a
CC therapeutically effective amount of a compound or agent which activates
CC the expression of mammalian KSR protein or a vector expressing mammalian
CC KSR; identifying compounds or agents which inhibit the expression of KSR,
CC by incubating a cell expressing KSR in the presence and absence of a
CC candidate compound or agent, and detecting or measuring the expression of
CC KSR in the presence and absence of a candidate compound or agent, where a
CC decrease in the expression of KSR in the presence of the candidate
CC compound or agent versus in the absence of the candidate compound or
CC agent indicates that the compound or agent inhibits the expression of KSR
CC ; and a ribozyme that cleaves KSR mRNA. (I) is useful for inhibiting the
CC expression of mammalian KSR comprising contacting cells which express KSR
CC with (I), where expression of mammalian KSR is inhibited. (I) is useful
CC for conferring radiosensitivity to ionizing radiation in tumor cells in a
CC mammal. (I) is useful for inhibiting angiogenesis in a mammal. (I) is
CC useful for inhibiting or reducing VEGF expression or activity in a
CC mammal. The methods are useful for treating or preventing
CC hyperproliferative condition associated with expression of gf-Ras or
CC heightened expression of Ras in a mammal and for treating or inhibiting
CC the progression of cancer in a mammal. The cancer is chosen from
CC pancreatic cancer, lung cancer, skin cancer, urinary tract cancer,
CC bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal
CC cancer, leukemia, lymphoma, neuroblastoma, head and neck cancer, breast
CC cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate
CC cancer. The present sequence represents a KSR antisense oligonucleotide.
XX
SQ Sequence 18 BP; 1 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGACCTAGAGGCAAG 18
Db 18 CGGACCTAGAGGCAAG 1

DE	Kinase suppressor of Ras (KSR) antisense oligonucleotide, SEQ ID NO:25.
XX	
XX	Kinase suppressor of Ras; KSR, cytosolic; neoplasm; pancreas tumor;
KW	liver tumor; skin tumor; thyroid tumor; lung tumor; urinary tract tumor;
KW	gastrintestinal disease; respiratory disease; genitourinary disease;
KW	endocrine disease; bladder tumor; colon tumor; intestine tumor;
KW	head & neck tumor; leukemia; hematological disease; lymphoma;
KW	immune system tumor; esophagus tumor; breast tumor; stomach tumor;
KW	neurological disease; ovary tumor;
KW	gynecologic and obstetrics; ss; angiogenesis disorder; antiangiogenic;
KW	cardiovascular disease; antisense oligonucleotide; antisense therapy;
XX	prostate tumor; andrology; cancer; hyperproliferation.
OS	Homo sapiens.
OS	Mus sp.
OS	Synthetic.
XX	
FH	Key
FT	Location/Qualifiers
FT	1..120
FT	/tag=a
FT	/partial
FT	/product= "Kinase suppressor of Ras (KSR) fragment"
FT	/note= "No start or stop codon shown"
XX	
PN	WO2005056756-A2.
XX	
PD	23-JUN-2005.
XX	
PE	03-DEC-2004; 2004WO-US040506.
XX	
PR	03-DEC-2003; 2003US-00727358.
XX	
PA	(SLOK) SLOAN KETTERING INST CANCER RES.
XX	
PI	Kolesnicik RN, Xing HR;
XX	
DR	WPI: 2005-445165/45.
XX	
XX	P-PSDB; AEA46559.
PT	New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression,
PT	useful for inhibiting expression of mammalian KSR and treating
PT	hyperproliferative conditions such as lung cancer, skin cancer, and
PT	ovarian cancer.
PS	Claim 6; SEQ ID NO 25; 186bp; English.
XX	
CC	The invention relates to an oligonucleotide (I) which is substantially
CC	complementary to a region of kinase suppressor of Ras (KSR) RNA, where
CC	the oligonucleotide inhibits the expression of KSR. Also included are the
CC	following: an oligonucleotide (II) which is substantially complementary
CC	to a translation initiation site, 5' untranslated region, coding region
CC	or 3' untranslated region of mRNA encoding mammalian KSR; an antisense
CC	oligonucleotide (III) comprising a sequence substantially complementary
CC	to the 3' region of KSR; an antisense oligonucleotide (IV) comprising a
CC	sequence substantially complementary to nucleotides 124-243 of the coding
CC	sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion;
CC	an antisense oligonucleotide (V) comprising a sequence chosen from
CC	AEA46539, AEA46540 and AEA46541, and; a recombinant DNA molecule (VI)
CC	comprising a nucleic acid sequence which encodes on transcription an
CC	antisense RNA complementary to mammalian KSR RNA or its portion; a cell
CC	(VII) transfected with (VI); an expression vector (VI) capable of
CC	expressing a nucleic acid which is substantially complementary to the
CC	coding sequence of KSR RNA, or its portion/fragment, where the
CC	oligonucleotide/nucleic acid inhibits the expression of KSR; an
CC	expression vector (VI) capable of expressing an oligonucleotide which is
CC	substantially complementary to the 3' region of the coding sequence of
CC	KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the
CC	expression of KSR; a pharmaceutical composition (PCI) comprising (I) and
CC	a carrier or diluent; a composition (CI) comprising (I) and a carrier or
CC	diluent; a composition (C2) comprising one or more chemotherapeutic or
CC	radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA
CC	encoding mammalian KSR and which inhibits KSR expression; a composition

Query Match	100.0%	Score 18;	DB 14;	Length 121;
Best Local Similarity	100.0%	Pred. No. 22;		
Matches 18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
DB	91	CGAGCCTTAGCGCAAG	108	
02	1	CGAGCCTTAGCGCAAG	18	
RESULT 8				
AEA46557				
AEA46557 standard; cDNA; 2601 BP.				
XX	AEA46557;			
XX	25-AUG-2005	(first entry)		
DB	Human kinase suppressor of Ras 1 (KSR1) cDNA.			
XX	gene; Kinase suppressor of Ras; KSR; cytosolic; neoplasm;			
KW	pancreas tumor; liver tumor; skin tumor; thyroid tumor; lung tumor;			
KW	urinary tract tumor; gastrointestinal disease; respiratory disease;			
KW	genitourinary disease; endocrine disease; bladder tumor; colon tumor;			

KM intestine tumor; head & neck tumor; leukemia; hematological disease;
 KM lymphoma; immune disorder; esophagus tumor; breast tumor; stomach tumor;
 KM nervous system tumor; neurological disease; ovary tumor;
 KM gynecology and obstetrics; ss; angiogenesis disorder; antiangiogenic;
 KM cardiovascular disease; antisense therapy; prostate tumor; andrology;
 KM cancer; hyperproliferation.
 XX
 OS Homo sapiens.
 XX
 PN MO2005056756-A2.
 XX
 PD 23-JUN-2005.
 XX
 PF 03-DEC-2004; 2004MO-US040506.
 XX
 PR 03-DEC-2003; 2003US-00727358.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX
 PI Kolesnick RN, Xing HR;
 XX
 DR WPI; 2005-445165/45.
 XX
 PT New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression,
 PT useful for inhibiting expression of mammalian KSR and treating
 PT hyperproliferative conditions such as lung cancer, skin cancer, and
 PT ovarian cancer.
 XX
 PS Example 5; SEQ ID NO 24; 186pp; English.
 XX
 CC The invention relates to an oligonucleotide (I) which is substantially
 CC complementary to a region of kinase suppressor of Ras (KSR) RNA, where
 CC the oligonucleotide inhibits the expression of KSR. Also included are the
 CC following: an oligonucleotide (II) which is substantially complementary
 CC to a translation initiation site, 5' untranslated region, coding region
 CC or 3' untranslated region of mRNA encoding mammalian KSR; an antisense
 CC oligonucleotide (III) comprising a sequence substantially complementary
 CC to the CAl region of KSR; an antisense oligonucleotide (IV) comprising a
 CC sequence substantially complementary to nucleotides 124-243 of the coding
 CC sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion;
 CC an antisense oligonucleotide (V) comprising a sequence chosen from
 CC AEA46539, AEA46540 and AEA46541, and ; a recombinant DNA molecule (VI)
 CC comprising a nucleic acid sequence which encodes on transcription an
 CC antisense RNA complementary to mammalian KSR RNA or its portion; a cell
 CC (VII) transfected with (VI); an expression vector (VI) capable of
 CC expressing a nucleic acid which is substantially complementary to the
 CC coding sequence of KSR RNA, or its portion/fragment, where the
 CC oligonucleotide/nucleic acid inhibits the expression of KSR; an
 CC expression vector (V2) capable of expressing an oligonucleotide which is
 CC substantially complementary to the CAl region of the coding sequence of
 CC KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the
 CC expression of KSR; a pharmaceutical composition (PCI) comprising (I) and
 CC a carrier or diluent; a composition (CI) comprising (I) and a carrier or
 CC diluent; a composition (C2) comprising one or more chemotherapeutic or
 CC radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA
 CC encoding mammalian KSR and which inhibits KSR expression; a composition
 CC (C3) comprising an expression vector and a carrier or diluent, where the
 CC expression vector is capable of expressing nucleic acid which is
 CC substantially complementary to the coding sequence of KSR RNA, or its
 CC portion/fragment, where the nucleic acid inhibits the expression of KSR;
 CC inhibiting (M1) the expression of mammalian KSR comprising contacting
 CC cells which express KSR with a nucleic acid which is complementary to a
 CC portion of the mRNA encoding KSR; treating or preventing (M2) a
 CC hyperproliferative condition associated with the expression of gf-Ras or
 CC heightened expression of Ras in a mammal comprising administering to the
 CC mammal a compound or agent which inhibits the expression of mammalian KSR
 CC protein; treating or preventing (M3) a hyperproliferative condition
 CC associated with the expression of gf-Ras or heightened expression of Ras
 CC in a mammal comprising expressing in the mammal or administering to the
 CC mammal therapeutically effective amount of a nucleic acid which is
 CC complementary to a portion of the mRNA encoding KSR; treating or
 CC inhibiting (M4) the progression of cancer in a mammal comprising
 CC administering to a mammal a compound or agent which inhibits the

CC expression of mammalian KSR protein; inhibiting angiogenesis of tumor
 CC cells in a mammal, by administering to a mammal a compound or agent which
 CC inhibits the expression of mammalian KSR protein; inhibiting or reducing
 CC VEGF expression or activity in a mammal, by administering a compound or
 CC agent that inhibits the expression of mammalian KSR protein; stimulating
 CC angiogenesis in a mammal comprising administering to a mammal a
 CC therapeutically effective amount of a compound or agent which activates
 CC the expression of mammalian KSR protein or a vector expressing mammalian
 CC KSR; identifying compounds or agents which inhibit the expression of KSR,
 CC by incubating a cell expressing KSR in the presence and absence of a
 CC candidate compound or agent, and detecting or measuring the expression of
 CC KSR in the presence and absence of a candidate compound or agent, where a
 CC decrease in the expression of KSR in the presence of the candidate
 CC compound or agent versus in the absence of the candidate compound or
 CC agent indicates that the compound or agent inhibits the expression of KSR
 CC ; and a ribozyme that cleaves KSR mRNA. (I) Is useful for inhibiting the
 CC expression of mammalian KSR comprising contacting cells which express KSR
 CC with (I), where expression of mammalian KSR is inhibited. (I) Is useful
 CC for conferring radiosensitivity to ionizing radiation in tumor cells in a
 CC mammal. (I) Is useful for inhibiting angiogenesis in a mammal. (I) Is
 CC useful for inhibiting or reducing VEGF expression or activity in a
 CC mammal. The methods are useful for treating or preventing
 CC hyperproliferative condition associated with expression of gf-Ras or
 CC heightened expression of Ras in a mammal and for treating or inhibiting
 CC the progression of cancer in a mammal. The cancer is chosen from
 CC pancreatic cancer, lung cancer, skin cancer, urinary tract cancer,
 CC bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal
 CC cancer, leukemia, lymphoma, neuroblastoma, head and neck cancer, breast
 CC cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate
 CC cancer. The present sequence represents human KSR1 cDNA.
 XX
 SQ Sequence 2601 BP, 565 A, 818 C, 772 G, 446 T, 0 U, 0 Other;
 XX
 QY 1 CGAGCCTTAGAGGCAAG 18
 DB 187 CGAGCCTTAGAGGCAAG 204
 XX
 RESULT 9
 AEA46544
 ID AEA46544 standard; cDNA; 4034 BP.
 XX
 AC AEA46544;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE Mouse kinase suppressor of Ras (KSR) cDNA.
 XX
 KW gene; Kinase suppressor of Ras; KSR; cytosolic; neoplasm;
 KW pancreas tumor; liver tumor; skin tumor; thyroid tumor; lung tumor;
 KW urinary tract tumor; gastrointestinal disease; respiratory disease;
 KW genitourinary disease; endocrine disease; bladder tumor; colon tumor;
 KW intestine tumor; head & neck tumor; leukemia; hematological disease;
 KW lymphoma; immune disorder; esophagus tumor; breast tumor;
 KW nervous system tumor; neurological disease; ovary tumor;
 KW gynecology and obstetrics; ss; angiogenesis disorder; antiangiogenic;
 KW cardiovascular disease; antisense therapy; prostate tumor; andrology;
 KW cancer; hyperproliferation.
 XX
 OS Mus sp.
 XX
 FH Key location/Qualifiers
 FT CDS 83..2704
 FT /tag= a
 FT /product= "Mouse kinase suppressor of Ras (KSR)"
 XX
 PN MO2005056756-A2.
 XX
 PD 23-JUN-2005.

XX 03-DEC-2004; 2004WO-US040506.
 XX 03-DEC-2003; 2003US-00727358.
 XX (SLOK) SLOAN KETTERING INST CANCER RES.
 XX Kolesnick RN, Xing HR;
 XX MPI; 2005-445165/45.
 XX P-PSDB; AEA46542.
 DR New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression,
 PT useful for inhibiting expression of mammalian KSR and treating
 PT hyperproliferative conditions such as lung cancer, skin cancer, and
 PT ovarian cancer.
 XX Disclosure; SEQ ID NO 11; 186pp; English.
 XX The invention relates to an oligonucleotide (I) which is substantially
 CC complementary to a region of kinase suppressor of Ras (KSR) RNA, where
 CC the oligonucleotide inhibits the expression of KSR. Also included are the
 CC following: an oligonucleotide (II) which is substantially complementary
 CC to a translation initiation site, 5' untranslated region, coding region
 CC or 3' untranslated region of mRNA encoding mammalian KSR; an antisense
 CC oligonucleotide (III) comprising a sequence substantially complementary
 CC to the CAl region of KSR; an antisense oligonucleotide (IV) comprising a
 CC sequence substantially complementary to nucleotides 124-243 of the coding
 CC sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion;
 CC an antisense oligonucleotide (V) comprising a sequence chosen from
 CC AEA46539, AEA46540 and AEA46541, and ; a recombinant DNA molecule (VI)
 CC comprising a nucleic acid sequence which encodes on transcription an
 CC antisense RNA complementary to mammalian KSR RNA or its portion; a cell
 CC (VII) transfected with (VI); an expression vector (VI) capable of
 CC expressing a nucleic acid which is substantially complementary to the
 CC coding sequence of KSR RNA, or its portion/fragment, where the
 CC oligonucleotide/nucleic acid inhibits the expression of KSR; an
 CC expression vector (V2) capable of expressing an oligonucleotide which is
 CC substantially complementary to the CAl region of the coding sequence of
 CC KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the
 CC expression of KSR; a pharmaceutical composition (PC1) comprising (I) and a
 CC carrier or diluent; a composition (C2) comprising one or more chemotherapeutic
 CC or radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA
 CC encoding mammalian KSR and which inhibits KSR expression; a composition
 CC (C3) comprising an expression vector and a carrier or diluent, where the
 CC expression vector is capable of expressing nucleic acid which is
 CC substantially complementary to the coding sequence of KSR RNA, or its
 CC portion/fragment, where the nucleic acid inhibits the expression of KSR;
 CC inhibiting (M1) the expression of mammalian KSR comprising contacting
 CC cells which express KSR with a nucleic acid which is complementary to a
 CC portion of the mRNA encoding KSR; treating or preventing (M2) a
 CC hyperproliferative condition associated with the expression of gf-Ras or
 CC heightened expression of Ras in a mammal comprising administering to the
 CC mammal a compound or agent which inhibits the expression of mammalian KSR
 CC protein; treating or preventing (M3) a hyperproliferative condition
 CC associated with the expression of gf-Ras or heightened expression of Ras
 CC in a mammal comprising expressing in the mammal or administering to the
 CC mammal therapeutically effective amount of a nucleic acid which is
 CC complementary to a portion of the mRNA encoding KSR; treating or
 CC inhibiting (M4) the progression of cancer in a mammal comprising
 CC administering to a mammal a compound or agent which inhibits the
 CC expression of mammalian KSR protein; inhibiting angiogenesis of tumor
 CC cells in a mammal, by administering to a mammal a compound or agent which
 CC inhibits the expression of mammalian KSR protein; inhibiting or reducing
 CC VEGF expression or activity in a mammal, by administering a compound or
 CC agent that inhibits the expression of mammalian KSR protein; stimulating
 CC angiogenesis in a mammal comprising administering to a mammal a
 CC therapeutically effective amount of a compound or agent which activates
 CC the expression of mammalian KSR protein or a vector expressing mammalian
 CC KSR; identifying compounds or agents which inhibit the expression of KSR,
 CC by incubating a cell expressing KSR in the presence and absence of a
 CC candidate compound or agent, and detecting or measuring the expression of

CC KSR in the presence and absence of a candidate compound or agent, where a
 CC decrease in the expression of KSR in the presence of the candidate
 CC compound or agent versus in the absence of the candidate compound or
 CC agent indicates that the compound or agent inhibits the expression of KSR
 CC ; and a ribozyme that cleaves KSR mRNA. (I) Is useful for inhibiting the
 CC expression of mammalian KSR comprising contacting cells which express KSR
 CC with (I), where expression of mammalian KSR is inhibited. (I) Is useful
 CC for conferring radiosensitivity to ionizing radiation in tumor cells in a
 CC mammal. (I) Is useful for inhibiting angiogenesis in a mammal. (I) Is
 CC useful for inhibiting or reducing VEGF expression or activity in a
 CC mammal. The methods are useful for treating or preventing
 CC hyperproliferative condition associated with expression of gf-Ras or
 CC heightened expression of Ras in a mammal and for treating or inhibiting
 CC the progression of cancer in a mammal. The cancer is chosen from
 CC pancreatic cancer, lung cancer, skin cancer, urinary tract cancer,
 CC bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal
 CC cancer, leukemia, lymphoma, neuroblastoma, head and neck cancer, breast
 CC cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate
 CC cancer. The present sequence represents mouse KSR cDNA.
 XX Sequence 4034 BP; 906 A; 1200 C; 1171 G; 757 T; 0 U; 0 Other;
 XX
 XX Query Match 100.0%; Score 18; DB 14; Length 4034;
 XX Best Local Similarity 100.0%; Pred. No. 25;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 CGGACCTTACGCGCAAG 18
 XX |||||
 XX 296 CGGACCTTACGCGCAAG 313
 XX
 XX RESULT 10
 XX AAT72155
 XX ID AAT72155 standard; cDNA; 4094 BP.
 XX AC AAT72155;
 XX DT 13-SEP-1997 (first entry)
 XX DE Mouse Ksr-1 (Kinase suppressor of Ras) cDNA.
 XX KM Kinase suppressor of Ras; Ksr-1; signal transduction; cell growth;
 XX cell differentiation; gene therapy; diagnosis; de.
 XX OS Mus musculus.
 XX FH Key Location/Qualifiers
 XX FT CDS 83..2704
 XX /*tag= a
 XX
 XX PN W09721820-A2.
 XX PD 19-JUN-1997.
 XX PF 13-DEC-1996; 96WO-US019941.
 XX PR 13-DEC-1995; 95US-00571758.
 XX XX (REGC) UNIV CALIFORNIA.
 XX PI Rubin G, Therrien M, Chang H, Karim F, Maassarman D;
 XX WP1; 1997-332791/30.
 XX DR P-PSDB; AAW19918.
 XX PT Isolated kinase suppressor of ras protein - used to identify lead
 XX compounds and in diagnosis or treatment of disease associated with Ksr
 XX activity or Ksr signal transduction.
 XX PS Claim 5; Page 32-34; 49pp; English.
 XX A cDNA clone (AAT72155) includes a complete open reading frame that codes
 CC for mouse kinase suppressor of Ras (AAW19918) designated Ksr-1, a novel

CC protein kinase involved in the regulation of cell growth and
 CC differentiation. It was isolated from a mouse PC4 teratocarcinoma cell
 CC line with a probe corresponding to hb, a sequence that had been
 CC identified as showing similarity to Drosophila melanogaster Ksr (see also
 CC AAT72153). Drosophila virilis and human Ksr sequences (see also AAT72154,
 CC AAT82156-57) have also been identified. These Ksr homologues define a
 CC novel class of kinases related to raf kinases. Ksr nucleic acids can be
 CC used to produce Ksr polypeptides, as probes to identify mutant Ksr
 CC alleles associated with disease, and in gene therapy applications
 CC
 XX Sequence 4094 BP; 924 A; 1212 C; 1193 G; 765 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 4094;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 CGGACCTTAGAGCGCAAG 18
 DB 296 CGGACCTTAGAGCGCAAG 313

RESULT 11

ADG75394 ID ADG75394 standard; cDNA; 4094 BP.

XX ADG75394;

DT 11-MAR-2004 (first entry)

XX Mouse kinase suppressor of Ras (KSR) coding sequence.

KW antisense oligonucleotide; kinase suppressor of Ras; KSR; cancer;
 KW pancreatic cancer; lung cancer; skin cancer; urinary tract cancer;
 KW bladder cancer; liver cancer; thyroid cancer; colon cancer;
 KW intestinal cancer; breast cancer; ovarian cancer; stomach cancer;
 KW head cancer; neck cancer; oesophageal cancer; prostate cancer; leukaemia;
 KW lymphoma; neuroblastoma; mouse; murine; gene; ss.

XX Mus sp.

PN MO2003101386-A2.

XX 11-DEC-2003.

PF 29-MAY-2003; 2003MO-US016961.

XX 30-MAY-2002; 2002US-0384228P.

PR 03-APR-2003; 2003US-0460023P.

(SLOK) SLOAN KETTERING INST CANCER RES.

XX Kolesnick RN, Xing HR;

XX WPI; 2004-053335/05.

DR P-PSDB; ADG75392.

XX New antisense oligonucleotides complementary to a region of kinase
 PT suppressor of Ras (KSR) RNA which inhibit KSR expression, useful for
 PT treating or inhibiting progression of cancer, e.g. pancreatic, lung,
 PT skin, or bladder cancer.

XX Example 1; SEQ ID NO 11; 120bp; English.

XX The invention comprises antisense oligonucleotides which are designed to
 CC inhibit the expression of the kinase suppressor of Ras (KSR) gene. The
 CC antisense oligonucleotides of the invention are useful for treating or
 CC inhibiting the progression of cancer, such as: pancreatic cancer, lung
 CC cancer, skin cancer, urinary tract cancer, bladder cancer, liver cancer,
 CC thyroid cancer, colon cancer, intestinal cancer, breast cancer, ovarian
 CC cancer, stomach cancer, head and neck cancer, oesophageal cancer,
 CC prostate cancer, leukaemia, lymphoma, and neuroblastoma. The present cDNA
 CC sequence encodes the mouse KSR protein.

SQ Sequence 4094 BP; 924 A; 1212 C; 1193 G; 765 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 4094;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 CGGACCTTAGAGCGCAAG 18
 DB 296 CGGACCTTAGAGCGCAAG 313

RESULT 12

AE46541/C ID AE46541 standard; DNA; 16 BP.

XX AE46541;

DT 25-AUG-2005 (first entry)

XX Kinase suppressor of Ras (KSR) antisense oligonucleotide, SEQ ID NO:8.

KW kinase suppressor of Ras; KSR; cytostatic; neoplasm; pancreas tumor;
 KW liver tumor; skin tumor; thyroid tumor; lung tumor; urinary tract tumor;
 KW gastrointestinal disease; respiratory disease; genitourinary disease;
 KW endocrine disease; bladder tumor; colon tumor; intestine tumor;
 KW head & neck tumor; leukemia; hematological disease; lymphoma;
 KW immune disorder; esophagus tumor; breast tumor; stomach tumor;
 KW nervous system tumor; neurological disease; ovary tumor;
 KW gynecology and obstetrics; ss; angiogenesis disorder; antiangiogenic;
 KW cardiovascular disease; antisense oligonucleotide; antisense therapy;
 KW prostate tumor; andrology; cancer; hyperproliferation.

XX Homo sapiens.

OS Mus sp.

PN WO2005056756-A2.

XX 23-JUN-2005.

PF 03-DEC-2004; 2004MO-US040506.

PR 03-DEC-2003; 2003US-00727358.

(SLOK) SLOAN KETTERING INST CANCER RES.

XX Kolesnick RN, Xing HR;

XX WPI; 2005-445165/45.

XX New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression,
 PT useful for inhibiting expression of mammalian KSR and treating
 PT hyperproliferative conditions such as lung cancer, skin cancer, and
 PT ovarian cancer.

XX Claim 8; SEQ ID NO 8; 186bp; English.

XX The invention relates to an oligonucleotide (I) which is substantially
 CC complementary to a region of kinase suppressor of Ras (KSR) RNA, where
 CC the oligonucleotide inhibits the expression of KSR. Also included are the
 CC following: an oligonucleotide (II) which is substantially complementary
 CC to a translation initiation site, 5' untranslated region, coding region
 CC or 3' untranslated region of mRNA encoding mammalian KSR; an antisense
 CC oligonucleotide (III) comprising a sequence substantially complementary
 CC to the 3'UTR of KSR; an antisense oligonucleotide (IV) comprising a
 CC sequence substantially complementary to nucleotides 124-243 of the coding
 CC sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion;
 CC an antisense oligonucleotide (V) comprising a sequence chosen from
 CC AE46539, AE46540 and AE46541, and; a recombinant DNA molecule (VI)
 CC comprising a nucleic acid sequence which encodes on transcription an
 CC antisense RNA complementary to mammalian KSR RNA or its portion; a cell
 CC (VII) transfected with (VI); an expression vector (VI) capable of
 CC expressing a nucleic acid which is substantially complementary to the

CC coding sequence of KSR RNA, or its portion/fragment, where the
CC oligonucleotide/nucleic acid inhibits the expression of KSR; an
CC expression vector (V2) capable of expressing an oligonucleotide which is
CC substantially complementary to the CAl region of the coding sequence of
CC KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the
CC expression of KSR; a pharmaceutical composition (PC1) comprising (1) and
CC a carrier or diluent; a composition (C1) comprising (1) and a carrier or
CC diluent; a composition (C2) comprising one or more chemotherapeutic or
CC radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA
CC encoding mammalian KSR and which inhibits KSR expression; a composition
CC (C3) comprising an expression vector and a carrier or diluent, where the
CC expression vector is capable of expressing nucleic acid which is
CC substantially complementary to the coding sequence of KSR RNA, or its
CC portion/fragment, where the nucleic acid inhibits the expression of KSR;
CC inhibiting (M1) the expression of mammalian KSR comprising contacting
CC cells which express KSR with a nucleic acid which is complementary to a
CC portion of the mRNA encoding KSR; treating or preventing (M2) a
CC hyperproliferative condition associated with the expression of gf-Ras or
CC heightened expression of Ras in a mammal comprising administering to the
CC mammal a compound or agent which inhibits the expression of mammalian KSR
CC protein; treating or preventing (M3) a hyperproliferative condition
CC associated with the expression of gf-Ras or heightened expression of Ras
CC in a mammal comprising expressing in the mammal or administering to the
CC mammal therapeutically effective amount of a nucleic acid which is
CC complementary to a portion of the mRNA encoding KSR; treating or
CC inhibiting (M4) the progression of cancer in a mammal comprising
CC administering to a mammal a compound or agent which inhibits the
CC expression of mammalian KSR protein; inhibiting angiogenesis of tumor
CC cells in a mammal, by administering to a mammal a compound or agent which
CC inhibits the expression of mammalian KSR protein; inhibiting or reducing
CC VEGF expression or activity in a mammal, by administering a compound or
CC agent that inhibits the expression of mammalian KSR protein; stimulating
CC angiogenesis in a mammal comprising administering to a mammal a
CC therapeutically effective amount of a compound or agent which activates
CC the expression of mammalian KSR protein or a vector expressing mammalian
CC KSR; identifying compounds or agents which inhibit the expression of KSR,
CC by incubating a cell expressing KSR in the presence and absence of a
CC candidate compound or agent, and detecting or measuring the expression of
CC KSR in the presence and absence of a candidate compound or agent, where a
CC decrease in the expression of KSR in the presence of the candidate
CC compound or agent versus in the absence of the candidate compound or
CC agent indicates that the compound or agent inhibits the expression of KSR
CC; and a ribozyme that cleaves KSR mRNA. (1) Is useful for inhibiting the
CC expression of mammalian KSR comprising contacting cells which express KSR
CC with (1), where expression of mammalian KSR is inhibited. (1) Is useful
CC for conferring radiosensitivity to ionizing radiation in tumor cells in a
CC mammal. (1) Is useful for inhibiting angiogenesis in a mammal. (1) Is
CC useful for inhibiting or reducing VEGF expression or activity in a
CC mammal. The methods are useful for treating or preventing
CC hyperproliferative condition associated with expression of gf-Ras or
CC heightened expression of Ras in a mammal and for treating or inhibiting
CC the progression of cancer in a mammal. The cancer is chosen from
CC pancreatic cancer, lung cancer, skin cancer, urinary tract cancer,
CC bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal
CC cancer, leukemia, lymphoma, neuroblastoma, head and neck cancer, breast
CC cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate
CC cancer. The present sequence represents a KSR antisense oligonucleotide.
XX

Seq Sequence 16 BP; 1 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 88.9%; Score 16; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACCTAGAGCAAG 18
DB 16 GACCTAGAGCAAG 1

RESULT 13
ABL67488/C
ID ABL67488 standard; DNA; 376 BP.
XX

AC ABL67488;
XX
DT 15-MAY-2002 (first entry)
XX
DE Thyroid cancer related gene sequence SEQ ID NO:5825.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumor; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237315P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
XX (AVAL-) AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
XX Sopet DR, Weaver Z;
XX WPI: 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.

PS Claim 1; SEQ ID NO 5825; 44pp; English.

XX The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour

CC Sequence 376 BP; 78 A; 132 C; 76 G; 90 T; 0 U; 0 Other;

CC Query Match 85.6%; Score 15.4; DB 6; Length 376;

CC Best Local Similarity 94.1%; Pred. No. 5.1e+02;

CC Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18

DB 107 GGACCTAGAGGCAAG 91

RESULT 14

ABL69201/c

ID ABL69201 standard; DNA; 376 BP.

XX ABL69201;

XX 15-MAY-2002 (first entry)

DT Prostate cancer related gene sequence SEQ ID NO:7538.

DE Human: Cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

XX stomach; lung; prostate; pancreas; carcinoma; antitumour; carcinous;

KW cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;

KM gene; ds.

XX Homo sapiens.

OS

XX

XX PN MO200194629-A2.

PD 13-DEC-2001.

XX

XX 30-MAY-2001; 2001WO-US010838.

PF

XX

PR 05-JUN-2000; 2000US-0209473P.

PR 05-JUN-2000; 2000US-0209531P.

PR 18-SEP-2000; 2000US-0233133P.

PR 18-SEP-2000; 2000US-0233617P.

PR 20-SEP-2000; 2000US-0234009P.

PR 20-SEP-2000; 2000US-0234034P.

PR 20-SEP-2000; 2000US-0234052P.

PR 22-SEP-2000; 2000US-0234509P.

PR 22-SEP-2000; 2000US-0234567P.

PR 25-SEP-2000; 2000US-0234923P.

PR 25-SEP-2000; 2000US-0234924P.

PR 25-SEP-2000; 2000US-0235077P.

PR 25-SEP-2000; 2000US-0235082P.

PR 25-SEP-2000; 2000US-0235134P.

PR 25-SEP-2000; 2000US-0235280P.

PR 26-SEP-2000; 2000US-0235637P.

PR 26-SEP-2000; 2000US-0235638P.

PR 27-SEP-2000; 2000US-0235711P.

PR 27-SEP-2000; 2000US-0235720P.

PR 27-SEP-2000; 2000US-0235840P.

PR 27-SEP-2000; 2000US-0235863P.

PR 28-SEP-2000; 2000US-0236028P.

PR 28-SEP-2000; 2000US-0236032P.

PR 28-SEP-2000; 2000US-0236033P.

PR 28-SEP-2000; 2000US-0236034P.

PR 28-SEP-2000; 2000US-0236109P.

PR 28-SEP-2000; 2000US-0236111P.

PR 29-SEP-2000; 2000US-0236842P.

PR 29-SEP-2000; 2000US-0236891P.

PR 02-OCT-2000; 2000US-0237122P.

PR 02-OCT-2000; 2000US-0237173P.

PR 02-OCT-2000; 2000US-0237278P.

PR 02-OCT-2000; 2000US-0237294P.

PR 02-OCT-2000; 2000US-0237295P.

PR 02-OCT-2000; 2000US-0237316P.

PR 03-OCT-2000; 2000US-0237425P.

PR 03-OCT-2000; 2000US-0237598P.

PR 03-OCT-2000; 2000US-0237604P.

PR 03-OCT-2000; 2000US-0237606P.

PR 03-OCT-2000; 2000US-0237608P.

PR 01-NOV-2000; 2000US-0244867P.

PR 01-NOV-2000; 2000US-0245084P.

XX

XX (AVAL-) AVALON PHARM.

XX

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;

PI Sopet DR, Weaver Z;

XX

XX WPI; 2002-188264/24.

XX

XX Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

PT

XX

PS Claim 1; SEQ ID NO 7538; 44pp; English.

XX

XX The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour

CC

XX

XX Sequence 376 BP; 78 A; 132 C; 76 G; 90 T; 0 U; 0 Other;

CC Query Match 85.6%; Score 15.4; DB 6; Length 376;

CC Best Local Similarity 94.1%; Pred. No. 5.1e+02;

CC Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18

DB 107 GGACCTAGAGGCAAG 91

RESULT 15

ADF80786/c

ID ADF80786 standard; DNA; 388 BP.

XX

XX ADF80786;

AC

XX 26-FEB-2004 (first entry)

XX Leukemia-related DNA sequence #1342.
DE Cytostatic; Gene therapy; Leukemia; ss.
XX
XX Unidentified.
OS
XX WO2003039443-A2.
FN
XX
XX 15-MAY-2003.
PD
XX
XX 04-NOV-2002; 2002WO-EP012303.
PF
XX 05-NOV-2001; 2001EP-00126244.
PR 30-APR-2002; 2002EP-00009758.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFER) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
XX
XX Haferlach T, Schoch C, Kern W, Kohlmann A, Schittger S, Dugas M;
PI Eils R, Brose B, Mergenthaler S;
XX WPI; 2003-505037/47.
DR
XX Determining the subtype of leukemia cells and whether a patient sample
PT contains leukemia cells or other cells, useful for treating leukemia,
PT comprises determining the expression profile of a group of markers in a
PT patient sample.
XX
XX Disclosure; SEQ ID NO 1342; 2938bp; English.
PS
XX The present invention relates to a method (M1) for determining the
CC subtype of leukemia cells and whether a patient sample contains
CC leukemia cells. The method comprises determining the expression profile
CC of a group of markers in a patient sample. The method is useful for
CC determining the presence of leukemia cells, its types or subtypes, and
CC for the preparation of a medicament for treating leukemia.
XX
XX Sequence 388 BP; 119 A; 91 C; 57 G; 121 T; 0 U; 0 Other;
SQ
OY 2 GGACCCCTAGAGGCAAG 18
DB 360 GGACCCCTAGAGGCAAG 344

Query Match 85.6%; Score 15.4; DB 10; Length 388;
Best Local Similarity 94.1%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 16
AAK88398/C
ID AAK88398 standard; cDNA; 514 BP.
XX
XX AAK88398;
AC
XX
XX 05-NOV-2001 (first entry)
DT
XX
XX Human digestive system antigen coding sequence SEQ ID NO: 714.
DE
XX Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ss.
XX
XX Homo sapiens.
OS
XX WO200155314-A2.
FN
XX
XX 02-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US001324.
PF

XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-MAR-2000; 2000US-0198123P.
PR 19-MAR-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
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PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
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PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234222P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.

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XX	PR	02-OCT-2000	2000US-0237038P
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XX	PR	05-DEC-2000	2000US-0251989P
XX	PR	06-DEC-2000	2000US-0251479P
XX	PR	06-DEC-2000	2000US-0251856P
XX	PR	08-DEC-2000	2000US-0251868P
XX	PR	08-DEC-2000	2000US-0251869P
XX	PR	08-DEC-2000	2000US-0251889P
XX	PR	11-DEC-2000	2000US-0251909P
XX	PR	11-DEC-2000	2000US-0254097P
XX	PR	05-JAN-2001	2001US-0259678P
XX	PA	(HUMA-) HUMAN GENOME SCI. INC.	
XX	PI	Rosen CA, Barash SC, Ruben SM,	
XX	DR	WPI: 2001-502630/55.	
XX	DR	P-PSDB: AAM92625.	
XX	PT	Polynucleotides encoding digestive system antigens, useful for	

PT		diagnosing, treating, preventing and/or prognostizing disorders of the
PT		digestive system, particularly cancer and cancer metastases.
XX		
PS		Claim 1; SEQ ID NO 714; 986pp; English.
XX		
CC		The present invention provides the protein and coding sequences of a
CC		number of human digestive system antigens. These can be used in the
CC		diagnosis, treatment and prevention of digestive system disorders,
CC		including cancer, Meckel's diverticulum, bacterial or parasitic
CC		infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC		ulcerative colitis. The present sequence is a cDNA encoding a digestive
CC		system antigen of the invention
XX		
SQ		Sequence 514 BP; 162 A; 115 C; 96 G; 141 T; 0 U; 0 Other;
Query Match		85.6%; Score 15.4; DB 4; Length 514;
Best Local Similarity		94.1%; Pred. No. 5.le+02;
Matches 16; Conservative		0; Mismatches 1; Indels 0; Gaps 0;
DY		2 GGACCTTAGAGGCAAG 18
Db		430 GGACCCTTAGAGGCCAAG 414
RESULT 17		
AAS39499/c		
ID	AAS39499 standard; cDNA; 514 BP.	
XX		
AC	AAS39499;	
XX		
DT	17-DEC-2001 (first entry)	
XX		
DE	cDNA encoding novel human colon associated polypeptide #152.	
XX		
KW	Human; colon cancer; congenital abnormality; infection; colitis;	
KW	inflammatory bowel disease; IBD; neoplastic disorder; gene therapy;	
KW	intestinal inflammatory disorder; malabsorption syndrome; gastric;	
KW	sigmoid disease; antibacterial; antiviral; antiinflammatory; cytostatic;	
ss.		
OS	Homo sapiens.	
XX		
PN	WO20015302-A2.	
XX		
PD	02-AUG-2001.	
XX		
PF	17-JAN-2001; 2001WO-US001240.	
PR	31-JAN-2000; 2000US-0179065P.	
PR	04-FEB-2000; 2000US-0180628P.	
PR	24-FEB-2000; 2000US-0184664P.	
PR	02-MAR-2000; 2000US-0186350P.	
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PR	18-APR-2000; 2000US-0198123P.	
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PR	30-JUN-2000; 2000US-0215135P.	
PR	07-JUL-2000; 2000US-0216647P.	
PR	07-JUL-2000; 2000US-0216880P.	
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PR	11-JUL-2000; 2000US-0217496P.	
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PR	14-AUG-2000; 2000US-0225213P.	
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PR	14-AUG-2000; 2000US-0225266P.	
PR	14-AUG-2000; 2000US-0225267P.	
PR	14-AUG-2000; 2000US-0225268P.	
PR	14-AUG-2000; 2000US-0225269P.	
PR	14-AUG-2000; 2000US-0225270P.	
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PR	14-AUG-2000; 2000US-0225278P.	
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PR	14-AUG-2000; 2000US-0225282P.	
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PR	14-AUG-2000; 2000US-0225292P.	
PR	14-AUG-2000; 2000US-0225293P.	
PR	14-AUG-2000; 2000US-0225294P.	
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PR	14-AUG-2000; 2000US-0225305P.</	

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PR	14-AUG-2000	2000US-02255758
PR	14-AUG-2000	2000US-02257588
PR	14-AUG-2000	2000US-02257599
PR	18-AUG-2000	2000US-02266219
PR	22-AUG-2000	2000US-02266797
PR	22-AUG-2000	2000US-02266888
PR	23-AUG-2000	2000US-02271827
PR	23-AUG-2000	2000US-02270099
PR	30-AUG-2000	2000US-02289249
PR	01-SEP-2000	2000US-02292877
PR	01-SEP-2000	2000US-02293433
PR	01-SEP-2000	2000US-02293448
PR	01-SEP-2000	2000US-02293454
PR	01-SEP-2000	2000US-02295099
PR	05-SEP-2000	2000US-02295433
PR	06-SEP-2000	2000US-02304377
PR	06-SEP-2000	2000US-02304388
PR	08-SEP-2000	2000US-02312422
PR	08-SEP-2000	2000US-02312433
PR	08-SEP-2000	2000US-02312443
PR	08-SEP-2000	2000US-02314133
PR	08-SEP-2000	2000US-02314143
PR	08-SEP-2000	2000US-02312080
PR	08-SEP-2000	2000US-02312081
PR	12-SEP-2000	2000US-02319688
PR	14-SEP-2000	2000US-02332397
PR	14-SEP-2000	2000US-02332398
PR	14-SEP-2000	2000US-02332399
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PR	14-SEP-2000	2000US-02332401
PR	14-SEP-2000	2000US-02333063
PR	14-SEP-2000	2000US-02333064
PR	14-SEP-2000	2000US-02333655
PR	21-SEP-2000	2000US-02342233
PR	21-SEP-2000	2000US-02342749
PR	25-SEP-2000	2000US-02349577
PR	25-SEP-2000	2000US-02349588
PR	25-SEP-2000	2000US-02354844
PR	27-SEP-2000	2000US-02358366
PR	27-SEP-2000	2000US-02358366
PR	29-SEP-2000	2000US-02363677
PR	29-SEP-2000	2000US-02363688
PR	29-SEP-2000	2000US-02363689
PR	29-SEP-2000	2000US-02363709
PR	02-OCT-2000	2000US-02370377
PR	02-OCT-2000	2000US-02370378
PR	02-OCT-2000	2000US-02370388
PR	02-OCT-2000	2000US-02370400
PR	13-OCT-2000	2000US-02393955
PR	13-OCT-2000	2000US-02393957
PR	20-OCT-2000	2000US-02418099
PR	20-OCT-2000	2000US-02418266
PR	20-OCT-2000	2000US-02418267
PR	20-OCT-2000	2000US-02418553
PR	20-OCT-2000	2000US-02417853
PR	20-OCT-2000	2000US-02417866
PR	20-OCT-2000	2000US-02417877
PR	20-OCT-2000	2000US-02418088
PR	08-NOV-2000	2000US-02464756
PR	08-NOV-2000	2000US-02464777
PR	08-NOV-2000	2000US-02464788
PR	08-NOV-2000	2000US-02465234
PR	08-NOV-2000	2000US-02465234
PR	08-NOV-2000	2000US-02465256
PR	08-NOV-2000	2000US-02465277

XX	08-NOV-2000;	200TUS-0246528P.
PR	08-NOV-2000;	200TUS-0246532P.
PR	08-NOV-2000;	200TUS-0246509P.
PR	08-NOV-2000;	200TUS-0246602P.
PR	08-NOV-2000;	200TUS-0246610P.
PR	08-NOV-2000;	200TUS-0246611P.
PR	08-NOV-2000;	200TUS-0246613P.
PR	17-NOV-2000;	200TUS-0249207P.
PR	17-NOV-2000;	200TUS-0249208P.
PR	17-NOV-2000;	200TUS-0249209P.
PR	17-NOV-2000;	200TUS-0249210P.
PR	17-NOV-2000;	200TUS-0249211P.
PR	17-NOV-2000;	200TUS-0249212P.
PR	17-NOV-2000;	200TUS-0249213P.
PR	17-NOV-2000;	200TUS-0249214P.
PR	17-NOV-2000;	200TUS-0249215P.
PR	17-NOV-2000;	200TUS-0249216P.
PR	17-NOV-2000;	200TUS-0249217P.
PR	17-NOV-2000;	200TUS-0249218P.
PR	17-NOV-2000;	200TUS-0249244P.
PR	17-NOV-2000;	200TUS-0249245P.
PR	17-NOV-2000;	200TUS-0249246P.
PR	17-NOV-2000;	200TUS-0249265P.
PR	17-NOV-2000;	200TUS-0249297P.
PR	17-NOV-2000;	200TUS-0249299P.
PR	17-NOV-2000;	200TUS-0249300P.
PR	01-DEC-2000;	200TUS-0250160P.
PR	01-DEC-2000;	200TUS-0250391P.
PR	05-DEC-2000;	200TUS-0251030P.
PR	05-DEC-2000;	200TUS-0251988P.
PR	05-DEC-2000;	200TUS-0256719P.
PR	06-DEC-2000;	200TUS-0251479P.
PR	08-DEC-2000;	200TUS-0251856P.
PR	08-DEC-2000;	200TUS-0251868P.
PR	08-DEC-2000;	200TUS-0251869P.
PR	08-DEC-2000;	200TUS-0251989P.
PR	08-DEC-2000;	200TUS-0251990P.
PR	11-DEC-2000;	200TUS-0254057P.
PR	05-JAN-2001;	200IUS-0259678P.
XX	(HUMA-) HUMAN GENOME SCI INC.	
PA		
PI	Rosen CA, Barash SC, Ruben SM;	
DR	WPI; 2001-465567/50.	
DR	P-PSDB; AAU22619.	
XX		
PT	Isolated polypeptide for treating, preventing and/or prognosing	
PT	disorders related to the colon including colon cancers and also for	
PT	testing and detection e.g. diagnosis.	
XX		
PS	Claim 4; SEQ ID NO 162; 562pp; English.	
XX		
CC	The present invention relates to the isolation of novel human colon	
CC	associated polypeptides (AAU22466-AAU22701), and the cDNA and genomic	
CC	sequences encoding for them. The sequences of the invention are useful in	
CC	the diagnosis, treatment, prevention and/or prognosis of disorders of the	
CC	colon including colon cancer, congenital abnormalities (e.g. atresia and	
CC	stenosis), bacterial and viral infections, inflammatory bowel disease	
CC	(IBD), neoplastic cell disorders (e.g. polyps and adenomas, intestinal	
CC	inflammatory disorders, colitis, colonic inflammation, diarrhoea and	
CC	dysentery, malabsorption syndromes (e.g. lactose intolerance), intestinal	
CC	obstruction and sigmoid diseases. The polynucleotide sequences of the	
CC	invention can also be used in gene therapy. AAC39148-AAS39591 represent	
CC	cDNA sequences encoding for the novel human colon associated polypeptides	
CC	of the invention. Note: The sequence data for this patent did not form	
CC	part of the printed specification, but was obtained in electronic format	
CC	directly from WIPO at ftp.wipo.int/pub/published_pat_sequences	
XX		
SQ	Sequence 514 BP; 162 A; 115 C; 96 G; 141 T; 0 U; 0 Other;	
Query Match	85.6%; Score 15.4; DB 5; Length 514;	
Best Local Similarity	94.1%; Pred. NO. 5.1e+02;	
Matches 16; Conservative	0; Mismatches 1; Indels 0; Gaps 0	

QY 2 GGACCTAGAGCAAG 18
Db 430 GGACCTAGAGCCAAG 414
RESULT 18
ADBS2225/c
ID ADB32225 standard; cDNA, 514 BP.
XX
AC ADB32225;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human novel colon related polypeptide CDNA SEQ ID NO 162.
XX
KM gene therapy; ss; gene; cancer; liver disorder; hepatitis;
KM neural disorder; Alzheimer's disease; human; colon.
XX
OS Homo sapiens.
PN US2003050231-A1.
XX
PD 13-MAR-2003.
XX
PF 17-JAN-2001; 2001US-00764872.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217486P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 25-SEP-2000; 2000US-0234999P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235835P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236328P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.

PR	17-NOV-2000;	2000US-0249265P.
PR	17-NOV-2000;	2000US-0249297P.
PR	17-NOV-2000;	2000US-0249299P.
PR	17-NOV-2000;	2000US-0249300P.
PR	01-DEC-2000;	2000US-0250160P.
PR	01-DEC-2000;	2000US-0250391P.
PR	05-DEC-2000;	2000US-0251030P.
PR	05-DEC-2000;	2000US-0251988P.
PR	05-DEC-2000;	2000US-0256719P.
PR	06-DEC-2000;	2000US-0251479P.
PR	08-DEC-2000;	2000US-0251856P.
PR	08-DEC-2000;	2000US-0251868P.
PR	08-DEC-2000;	2000US-0251869P.
PR	08-DEC-2000;	2000US-0251989P.
PR	08-DEC-2000;	2000US-0251990P.
PR	11-DEC-2000;	2000US-0254097P.
PR	05-JAN-2001;	2001US-0259678P.
XX		
PA	(ROSE/) ROSEN C A.	
PA	(RUBE/) RUBEN S M.	
PA	(BARA/) BARASH S C.	
XX		
PI	Rosen CA, Ruben SM, Barash SC;	
XX		
DR	WPI, 2003-625420/59.	
DR	P-PSDB; ADBJ2459.	
XX		
PT	New nucleic acid molecule, useful for preparing a medicament for	
PT	preventing, treating or ameliorating a medical condition e.g. cancer,	
PT	liver disorders or neural disorders.	
XX		
PS	Claim 3; SEQ ID NO 162; 216pp; English.	
XX		
CC	The invention relates to an isolated nucleic acid molecule encoding a	
CC	polypeptide. The nucleic acid is useful for preparing a medicament for	
CC	preventing, treating or ameliorating a medical condition e.g. cancer,	
CC	liver disorders such as hepatitis or neural disorders such as Alzheimer's	
CC	disease. The present sequence represents a human cDNA encoding a novel	
CC	colon related polypeptide. Note: The sequence data for this patent did	
CC	not form part of the printed specification but was obtained in electronic	
CC	format directly from USPTO at	
CC	seqdata.uspto.gov/sequence.html?DocID=20030050231.	
XX		
SQ	Sequence 514 BP; 162 A; 115 C; 96 G; 141 T; 0 U; 0 Other;	
XX		
Query Match	85.6%; Score 15.4; DB 9; Length 514;	
Best Local Similarity	94.1%; Pred. No. 5.1e+02;	
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	2 GGACCCTAGAGGCAAG 18	
DB	430 GGACCCTAGAGGCCAAG 414	
XX		
RESULT 19		
ADF82177/C		
ID	ADF82177 standard; DNA; 986 BP.	
XX		
AC	ADF82177;	
XX		
DT	26-FEB-2004 (first entry)	
XX		
DE	Leukemia-related DNA sequence #2733.	
XX		
KM	Cytostatic; Gene therapy; leukemia; ss.	
XX		
OS	Unidentified.	
XX		
PN	WO2003039443-A2.	
XX		
PD	15-MAY-2003.	
XX		
04-NOV-2002; 2002WO-EP012303.		
02		

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XX 05-NOV-2001; 2001EP-00126244.
PR 30-APR-2002; 2002EP-00009758.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UJLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFF/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
XX
PI Haferlach T, Schoch C, Kern W, Kohlmann A, Schnittger S, Dugas M;
PI Eils R, Broes B, Mergenthaler S;
XX
XX WPI; 2003-505037/47.
DR
XX
XX Determining the subtype of leukemia cells and whether a patient sample
PT contains leukemia cells or other cells, useful for treating leukemia,
PT comprises determining the expression profile of a group of markers in a
PT patient sample.
XX
XX Disclosure; SEQ ID NO 2733; 2938bp; English.
XX
XX The present invention relates to a method (M1) for determining the
CC subtype of leukemia cells and whether a patient sample contains
CC leukemia cells. The method comprises determining the expression profile
CC of a group of markers in a patient sample. The method is useful for
CC determining the presence of leukemia cells, its types or subtypes, and
CC for the preparation of a medicament for treating leukaemia.
XX
XX Sequence 986 BP; 269 A; 216 C; 206 G; 232 T; 0 U; 63 Other;
SQ
XX
XX Query Match 85.6%; Score 15.4; DB 10; Length 986;
XX Best Local Similarity 94.1%; Pred. NO. 5.2e+02;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0
OY 2 GGACCTGAGAGCAAG 18
DB 498 GGACCTTGAGGCCAAG 482
XX
XX
XX RESULT 20
XX ID ADQ24821/c
XX ADQ24821 standard; DNA; 1797 .BP.
XX AC ADQ24821;
XX
XX DT 26-AUG-2004 (first entry)
XX
XX DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7641.
XX
XX KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
XX ds.
XX
XX OS Homo sapiens.
XX
XX PN WO2004048938-A2.
XX
XX PD 10-JUN-2004.
XX
XX PF 26-NOV-2003; 2003WO-US038193.
XX
XX PR 26-NOV-2002; 2002US-0429739P.
XX
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX
XX PI Aziz N, Ginsburg WM, Zlotnick A;
XX
XX WPI; 2004-441208/41.
XX
XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.

```

XX Example 2; SEQ ID NO 7641; 210bp; English.
PS The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 1797 BP; 574 A; 340 C; 360 G; 523 T; 0 U; 0 Other;
XX
Query Match 85.6%; Score 15.4; DB 12; Length 1797;
Best Local Similarity 94.1%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GGACCTAGAGGCAAG 18
Db 502 GGACCTAGAGGCCAAG 486
XX
RESULT 21
ADQ18079
ID ADQ18079 standard; DNA; 9645 BP.
XX
AC ADQ18079;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 896.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
XX db.
XX
OS Homo sapiens.
XX
PN NC0004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003MO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PT Aziz N, Ginsburg WM, Zlotnick A;
XX WPI; 2004-441208/41.
XX
DR WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
XX of a gene in a first soft tissue sample and a normal soft tissue sample
XX and comparing the gene expression, also useful in treating soft tissue
XX sarcoma.
XX
PT Example 2; SEQ ID NO 896; 210bp; English.
XX
PS The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic

CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 9645 BP; 2115 A; 2895 C; 2715 G; 1920 T; 0 U; 0 Other;
XX
Query Match 85.6%; Score 15.4; DB 12; Length 9645;
Best Local Similarity 94.1%; Pred. No. 5.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GGACCTAGAGGCAAG 18
Db 319 GGACCTAGAGGCCAAG 335
XX
RESULT 22
ADZ59509/C
ID ADZ59509 standard; DNA; 20001 BP.
XX
AC ADZ59509;
XX
DT 30-JUN-2005 (first entry)
XX
DE Secondary hyperparathyroidism detection human polymorphic gene, CH13L1.
XX
KW secondary hyperparathyroidism; endocrine-gen.; antihypoid;
XX renal failure; nephrotropic; SNP detection;
XX single nucleotide polymorphism; SNP; gene; db; CH13L1.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation 10001
FT /tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN JP2005102601-A.
XX
PD 21-APR-2005.
XX
PF 30-SEP-2003; 2003JP-00341015.
XX
PR 30-SEP-2003; 2003JP-00341015.
XX
PA (HYDB-) HYDBITTO GENOMICS KK.
XX (JIKI-) UNIV JIKI.
XX
DR WPI; 2005-358641/37.
XX
XX Testing secondary hyperparathyroidism in chronic renal failure patient,
XX PT involves detecting variation in gene chosen from CACNA1C, CALCR1,
XX EGF, GFR1, GFRAL, GPR56 and GPRK6.
XX
PS Claim 4; SEQ ID NO 3; 138bp; Japanese.
XX
XX The invention relates to a novel method for testing secondary
XX hyperparathyroidism in a chronic renal failure patient. The method
XX involves detecting a variation in a gene chosen from CACNA1C, CALCR1,
XX CH13L1, EGF, GFR1, GFRAL, GPR56, GPRK6, IL10RA, IL10RB, IL12RB1, KCNJ14,
XX KCNJ1, ORCT14, PDGFRA, SCYB14, SLC12A1, SLC2A3, TGFBR3, TMEM1, CALCR,
XX IL17R, OSTF1, EGF, MET, TGFBI and VEGF, or detecting the base in a
XX polymorphism region existing in the vicinity of any one of the genes. The
XX invention further comprises a reagent or kit for testing secondary
XX hyperparathyroidism in a chronic renal failure patient. This
XX polynucleotide sequence represents the polymorphism containing human
XX CH13L1 gene of the invention.
XX
SQ Sequence 20001 BP; 4773 A; 5041 C; 5158 G; 5029 T; 0 U; 0 Other;
XX
Query Match 85.6%; Score 15.4; DB 14; Length 20001;
Best Local Similarity 94.1%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCTAGAGCAAG 18
 |||||
 Db 2601 GGACCCGAGGCAAG 2585

RESULT 23
 ID ADQ97998/C
 ADQ97998 standard; DNA; 22475 BP.
 AC ADQ97998;
 DT 07-OCT-2004 (first entry)

DE Human cancer associated sequence HDL1-038, SEQ ID 975.

XX Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human; ds.

XX Homo sapiens.

XX WO2004060304-A2.

XX 22-JUL-2004.

XX 22-DEC-2003; 2003WO-US041389.

XX 27-DEC-2002; 2002US-00330773.

XX (SAGR-) SAGRES DISCOVERY INC.

XX Morris DW, Malandro MS;

XX MPI; 2004-543781/52.

XX New isolated cancer associated nucleic acids comprising at least 10

XX contiguous nucleotides, useful for diagnosing, preventing and/or treating

XX cancers such as leukemia and lymphoma.

XX Claim 1; SEQ ID NO 975; 199pp; English.

XX The present invention relates to cancer associated sequences (ADQ97025-

XX ADQ98004). The sequences are useful for the diagnosis, prevention and/or

XX treatment of cancer, such as leukemia and lymphoma. Note: The sequence

XX data for this patent did not form part of the printed specification, but

XX was obtained in electronic format directly from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 22475 BP; 5898 A; 5414 C; 5434 G; 5709 T; 0 U; 20 Other;

Qy 2 GGACCTAGAGCAAG 18
 |||||
 Db 15390 GGACCTAGAGCAAG 15374

RESULT 24
 ID ADM69029
 ADM69029 standard; DNA; 191150 BP.

XX ADM69029;

XX 03-JUN-2004 (first entry)

XX Human platelet derived growth factor receptor alpha wild-type gDNA.

XX platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;

XX wild-type; type III receptor tyrosine kinase; RTK; ds; gene.

XX Homo sapiens.

Key	Location/Qualifiers
FT CDS	1..191150
FT	/*tag= b
FT	/product= "Human platelet derived growth factor receptor
FT	alpha wild-type protein"
FT	1..49
FT	/*tag= a
FT	/number= 1
FT	50..2330
FT	/*tag= c
FT	/number= 1
FT	2331..2648
FT	/*tag= d
FT	/number= 2
FT	2649..4902
FT	/*tag= e
FT	/number= 2
FT	4903..5163
FT	/*tag= f
FT	/number= 3
FT	5164..6154
FT	/*tag= g
FT	/number= 3
FT	6155..6285
FT	/*tag= h
FT	/number= 4
FT	6286..8524
FT	/*tag= i
FT	/number= 4
FT	8525..8696
FT	/*tag= j
FT	/number= 5
FT	8697..8787
FT	/*tag= k
FT	/number= 5
FT	8788..8977
FT	/*tag= l
FT	/number= 6
FT	8978..166510
FT	/*tag= m
FT	/number= 6
FT	166511..166626
FT	/*tag= n
FT	/number= 7
FT	166627..168271
FT	/*tag= o
FT	/number= 7
FT	168272..168398
FT	/*tag= p
FT	/number= 8
FT	168399..169414
FT	/*tag= q
FT	/number= 8
FT	169415..169608
FT	/*tag= r
FT	/number= 9
FT	169609..170408
FT	/*tag= s
FT	/number= 9
FT	170409..170503
FT	/*tag= t
FT	/number= 10
FT	170504..170718
FT	/*tag= u
FT	/number= 10
FT	170719..170851
FT	/*tag= v
FT	/number= 11
FT	170852..173265
FT	/*tag= w
FT	/number= 11
FT	173266..173370
FT	/*tag= x

FT /number= 12
FT intron 173371..173773
FT /*tag= y
FT /number= 12
FT exon 173774..173884
FT /*tag= z
FT /number= 13
FT intron 173885..174239
FT /*tag= aa
FT /number= 13
FT exon 174240..174393
FT /*tag= ab
FT /number= 14
FT intron 174394..176193
FT /*tag= ac
FT /number= 14
FT exon 176194..176360
FT /*tag= ad
FT /number= 15
FT intron 176361..181248
FT /*tag= ae
FT /number= 15
FT exon 181249..181364
FT /*tag= af
FT /number= 16
FT intron 181365..181718
FT /*tag= ag
FT /number= 16
FT exon 181719..181841
FT /*tag= ah
FT /number= 17
FT intron 181842..183307
FT /*tag= ai
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FT exon 183308..183419
FT /*tag= aj
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FT intron 184777..184886
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FT exon 184887..184992
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FT /number= 20
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FT /number= 20
FT exon 186191..186432
FT /*tag= ap
FT /number= 21
FT intron 186433..191002
FT /*tag= aq
FT /number= 21
FT exon 191003..191150
FT /*tag= ar
FT /number= 22
PN WO2003105773-A2.
XX
XX
XX 24-DEC-2003.
XX
XX 13-JUN-2003; 2003WO-US018901.
XX
XX 13-JUN-2002; 2002US-0389107P.
XX
XX 08-JAN-2003; 2003US-0438899P.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
PA (DAND) DANA FARBER CANCER INST. INC.

PA (BGM) BRIGHAM & WOMENS HOSPITAL.
PA (USGO) US DEPT. VETERANS AFFAIRS.
XX
XX Heinrich MC, Corless CL, Fletcher JA, Demetri GD;
XX
XX WPI; 2004-082052/08.
XX
XX P-PSDB; ADM69012.
XX
XX New isolated variant platelet derived growth factor alpha (PDGFRa)
XX
XX PDGFRa-mediated neoplasia in a mammal.
XX
XX Example 1; SEQ ID NO 19; 302pp; English.
XX
XX The invention relates to a novel isolated variant platelet derived growth
XX
XX factor receptor alpha (PDGFRa) polypeptide. The polypeptide of the
XX
XX invention is a type III receptor tyrosine kinase (RTK) and may be useful
XX
XX for screening for a compound that may influence PDGFRa-mediated neoplasia
XX
XX in a mammal. The current sequence is that of the human PDGFRa wild-type
XX
XX genomic DNA of the invention.
XX
XX
XX Sequence 191150 BP; 55223 A; 39036 C; 39352 G; 56412 T; 0 U; 1127 Other;
SQ
Query Match 85.6%; Score 15.4; DB 12; Length 191150;
Best Local Similarity 94.1%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GGACCTAGAGGCAAG 18
Db 117726 GGACCTAGAGGCAAG 117742
|||||
RESULT 25
ABZ07598
ID ABZ07598 standard; DNA; 50 BP.
XX
XX AC ABZ07598;
XX
XX 09-JAN-2003 (first entry)
XX
XX DE Human leukocyte gene expression profiling probe SEQ ID NO 7589.
XX
XX KW T7; leukocyte; gene expression profiling; allograft rejection;
XX
XX KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
XX
XX KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX
XX ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200257414-A2.
XX
XX PD 25-JUL-2002.
XX
XX PF 22-OCT-2001; 2001WO-US047856.
XX
XX PR 20-OCT-2000; 2000US-0241994P.
XX
XX PR 08-JUN-2001; 2001US-0296764P.
XX
XX PA (BIOC-) BIOCARDIA INC.
XX
XX PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX
XX PI Ly N, Woodward R, Quertermous T, Johnson F;
XX
XX DR WPI; 2002-636525/68.
XX
XX PT New system for leukocyte expression profiling, diagnosing a disease, or
XX
XX PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX PS Claim 1; Page 572; Opp; English.
XX
XX CC The invention relates to a system for detecting gene expression, which
XX
XX comprises one or two isolated DNA molecules that detect expression of a

CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (AB200010-AB208152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX

Sequence 50 BP; 12 A; 15 C; 11 G; 12 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAA 16
DB 18 GGACCTTAGAGGCAA 32

RESULT 26
ADP10220
ID ADP10220 standard; DNA; 50 BP.
XX
AC ADP10220;
XX
DT 12-AUG-2004 (first entry)
XX
DE 50-mer oligonucleotide marker probe of the invention #229.
XX
KM transplant rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
XX Homo sapiens.
XX WO2004042346-A2.
XX
PD 21-MAY-2004.
XX
PF 24-APR-2003; 2003WO-US012946.
XX
PR 24-APR-2002; 2002US-00131831.
XX
PR 20-DEC-2002; 2002US-00325899.
XX
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX
DR WPI; 2004-400724/37.
XX
XX
PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
PS Claim 2; SEQ ID NO 229; 1762bp; English.
XX
XX The present invention relates to diagnosing or monitoring transplant
XX rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX comprising detecting the expression level of one or more genes. The
XX methods, system and kits are useful in diagnosing or monitoring
XX transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX islet, lung, bone marrow or stem cell transplant rejection,
XX xenotransplant rejection or mechanical organ replacement rejection, in an
XX individual. The method is also useful in assessing the immune status of
XX an individual. The methods are also useful in diagnosing and monitoring
XX diseases that involve the immune system, e.g. rheumatoid arthritis, or
XX lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX viral, bacterial or fungal infection. The present sequence represents a
XX 50 mer oligonucleotide marker for diagnosis and monitoring of allograft

CC rejection and other disorders.
XX
SQ Sequence 50 BP; 12 A; 15 C; 11 G; 12 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAA 16
DB 18 GGACCTTAGAGGCAA 32

RESULT 27
AAI76987/C
ID AAI76987 standard; DNA; 51 BP.
XX

AC AAI76987;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:3928.
XX

Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KM protein therapy; vaccine; probe; diagnostic assay; detection;
KM quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032758.
XX
PR 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach M;
XX
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX

Claim 1; Page 1254; 2653bp; English.

AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (II) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples

Sequence 51 BP; 9 A; 12 C; 19 G; 11 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAA 16
 Db 17 GGACCTTAGAGGCAA 3

RESULT 28

AA176986/c
 ID AA176986 standard; DNA; 51 BP.

XX AA176986;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:3927.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KM protein therapy; vaccine; probe; diagnostic assay; detection;
 KM quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX MO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000MO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shimkete RA, Leach M;

XX WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and
 therapy.

XX Claim 1; Page 1253; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
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XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
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 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

RESULT 29
 ABQ95689
 ID ABQ95689 standard; DNA; 75 BP.

XX ABQ95689;

AC ABQ95689;

DT 28-OCT-2002 (first entry)

DE Tumour suppression-related oligonucleotide #1340.

XX Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic;
 KM tumour suppression; tumour reversion; apoptosis; viral resistance; human;
 KM viral infection; cell degeneration disease; neurodegeneration; ds;
 KM Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.

XX Homo sapiens.

XX FR2819824-A1.

XX 26-JUL-2002.

XX 23-JAN-2001; 2001FR-00000899.

XX 23-JAN-2001; 2001FR-00000899.

XX (MOLE-) MOLECULAR ENGINES LAB SA.

XX Telerman A, Amson R, Tuijnder M, Susini L;

XX WPI; 2002-610803/66.

XX New nucleic acid implicated e.g. in tumor suppression, useful for
 PT diagnosis of tumors, viral infection and cellular degeneration and for
 PT drug screening.

XX Claim 1; Page 375; 623pp; French.

XX The present invention relates to novel human nucleic acid sequences (I).

XX The present invention relates to novel human nucleic acid sequences (I).

XX The present invention relates to novel human nucleic acid sequences (I).

XX The present invention relates to novel human nucleic acid sequences (I).

XX The present invention relates to novel human nucleic acid sequences (I).

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XX The present invention relates to novel human nucleic acid sequences (I).

XX The present invention relates to novel human nucleic acid sequences (I).

XX The present invention relates to novel human nucleic acid sequences (I).

XX The present invention relates to novel human nucleic acid sequences (I).

XX Human secreted protein 5' EST, SEQ ID NO: 28900.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KM gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GEST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic; forensic; gene therapy and chromosome mapping procedures.

XX Claim 1; SEQ ID NO 28900; 71bp + Sequence Listing; English.

CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
 CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
 CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors

CC Sequence 163 BP; 35 A; 57 C; 41 G; 30 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 3; Length 163;

Best Local Similarity 100.0%; Pred No. 7.9e+02; Mismatches 0; Gaps 0;

Matches 15; Conservative 0; Indels 0;

OY 2 GGACCTAGAGGCAA 16
 |||||
 DB 148 GGACCTAGAGGCAA 162

Search completed: April 15, 2006, 20:26:40
 Job time : 692 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 18:12:40 ; Search time 418 Seconds

(without alignments)
173.447 Million cell updates/sec

Title: US-10-727-358-5

Perfect score: 18
Sequence: 1 cggacctagagcgaag 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters: 18562198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications NA.New:*
1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.4	85.6	539	9	US-10-301-480-55145 Sequence 55145, A
2	15.4	85.6	539	9	US-10-301-480-668554 Sequence 668554, A
3	15.4	85.6	574	6	US-09-925-065A-504327 Sequence 504327, A
4	15.4	85.6	738	6	US-09-925-065A-65294 Sequence 65294, A
5	15.4	85.6	738	6	US-09-925-065A-65295 Sequence 65295, A
6	15.4	85.6	738	6	US-09-925-065A-65296 Sequence 65296, A
7	15.4	85.6	738	6	US-10-301-480-166533 Sequence 166533, A
8	15.4	85.6	738	9	US-10-301-480-166534 Sequence 166534, A
9	15.4	85.6	738	9	US-10-301-480-166535 Sequence 166535, A
10	15.4	85.6	738	10	US-10-301-480-779942 Sequence 779942, A
11	15.4	85.6	738	10	US-10-301-480-779943 Sequence 779943, A
12	15.4	85.6	738	10	US-10-301-480-779944 Sequence 779944, A
13	15.4	85.6	1155	8	US-10-750-185-61166 Sequence 61166, A
14	15.4	85.6	1155	8	US-10-750-623-61166 Sequence 61166, A
15	15.4	85.6	1206	9	US-10-932-182A-2596 Sequence 2596, Ap
16	15.4	85.6	1206	9	US-10-932-182A-2596 Sequence 2596, Ap
17	15.4	85.6	1806	11	US-11-096-568A-33576 Sequence 33576, A
18	15.4	85.6	1862	11	US-11-096-568A-2408 Sequence 2408, Ap

C 19	15.4	85.6	8703	14	US-11-128-061-856 Sequence 856, App
C 20	15.4	85.6	8703	14	US-11-128-049-856 Sequence 856, App
C 21	15.4	85.6	22475	14	US-10-330-773-975 Sequence 975, App
C 22	15.4	85.6	100000	14	US-11-124-367A-5024 Sequence 5024, Ap
C 23	15.4	85.6	171732	14	US-11-121-086-98 Sequence 98, App1
C 24	15	83.3	19	12	US-11-101-244-1292346 Sequence 1292346, A
C 25	15	83.3	19	12	US-11-101-244-1292367 Sequence 1292367, A
C 26	15	83.3	19	13	US-11-083-784-1292346 Sequence 1292346, A
C 27	15	83.3	19	13	US-11-083-784-1292367 Sequence 1292367, A
C 28	15	83.3	22	8	US-10-310-914A-965984 Sequence 965984, A
C 29	15	83.3	640	6	US-09-925-065A-799050 Sequence 799050, A
C 30	15	83.3	640	6	US-09-925-065A-799051 Sequence 799051, A
C 31	15	83.3	640	6	US-09-925-065A-799052 Sequence 799052, A
C 32	15	83.3	669	6	US-09-925-065A-799053 Sequence 799053, A
C 33	15	83.3	669	6	US-09-925-065A-853128 Sequence 853128, A
C 34	14.8	82.2	588	6	US-09-925-065A-758596 Sequence 758596, A
C 35	14.8	82.2	588	6	US-09-925-065A-585830 Sequence 585830, A
C 36	14.8	82.2	588	6	US-09-925-065A-585831 Sequence 585831, A
C 37	14.8	82.2	588	6	US-09-925-065A-585832 Sequence 585832, A
C 38	14.8	82.2	588	6	US-09-925-065A-585833 Sequence 585833, A
C 39	14.8	82.2	594	6	US-09-925-065A-126082 Sequence 126082, A
C 40	14.8	82.2	594	10	US-10-301-480-836831 Sequence 836831, A
C 41	14.8	82.2	600	9	US-10-301-480-13872 Sequence 13872, A
C 42	14.8	82.2	600	9	US-10-301-480-13873 Sequence 13873, A
C 43	14.8	82.2	600	9	US-10-301-480-42155 Sequence 42155, A
C 44	14.8	82.2	600	10	US-10-301-480-627281 Sequence 627281, A
C 45	14.8	82.2	600	10	US-10-301-480-627282 Sequence 627282, A
C 46	14.8	82.2	624	6	US-09-925-065A-894131 Sequence 894131, A
C 47	14.8	82.2	626	6	US-09-925-065A-892552 Sequence 892552, A
C 48	14.8	82.2	635	6	US-09-925-065A-895023 Sequence 895023, A
C 49	14.8	82.2	635	6	US-09-925-065A-895023 Sequence 895023, A
C 50	14.8	82.2	728	8	US-10-750-623-56857 Sequence 56857, A
C 51	14.8	82.2	728	8	US-10-750-623-56857 Sequence 56857, A
C 52	14.8	82.2	728	8	US-10-750-623-56857 Sequence 56857, A
C 53	14.8	82.2	955	10	US-10-301-480-609397 Sequence 609397, A
C 54	14.8	82.2	955	10	US-10-301-480-609397 Sequence 609397, A
C 55	14.8	82.2	1010	8	US-10-750-185-56857 Sequence 56857, A
C 56	14.8	82.2	1010	8	US-10-750-185-56857 Sequence 56857, A
C 57	14.8	82.2	2026	8	US-10-750-185-44073 Sequence 44073, A
C 58	14.8	82.2	2026	8	US-10-750-185-44073 Sequence 44073, A
C 59	14.8	82.2	4932	14	US-11-124-367A-63 Sequence 63, App1
C 60	14.8	82.2	17410	14	US-11-051-5683 Sequence 5683, App1
C 61	14.8	82.2	101786	14	US-11-117-187-199 Sequence 199, App
C 62	14.8	82.2	11736	11	US-11-114-798-49 Sequence 49, App1
C 63	14.6	81.1	669	6	US-09-925-065A-853127 Sequence 853127, A
C 64	14.4	80.0	25	9	US-10-932-182A-34647 Sequence 34647, A
C 65	14.4	80.0	25	9	US-10-932-182A-34647 Sequence 34647, A
C 66	14.4	80.0	25	14	US-11-121-849-667101 Sequence 667101, A
C 67	14.4	80.0	30	8	US-10-310-914A-108083 Sequence 108083, A
C 68	14.4	80.0	201	8	US-10-995-561-67008 Sequence 67008, A
C 69	14.4	80.0	201	14	US-11-124-368A-18202 Sequence 18202, A
C 70	14.4	80.0	201	14	US-11-124-367A-11233 Sequence 11233, A
C 71	14.4	80.0	454	10	US-10-301-480-486111 Sequence 486111, A
C 72	14.4	80.0	454	10	US-10-301-480-486111 Sequence 486111, A
C 73	14.4	80.0	454	10	US-10-301-480-486112 Sequence 486112, A
C 74	14.4	80.0	454	10	US-10-301-480-1099520 Sequence 1099520, A
C 75	14.4	80.0	454	10	US-10-301-480-1099521 Sequence 1099521, A
C 76	14.4	80.0	588	9	US-10-301-480-209388 Sequence 209388, A
C 77	14.4	80.0	588	10	US-10-301-480-822797 Sequence 822797, A
C 78	14.4	80.0	570	10	US-10-301-480-493947 Sequence 493947, A
C 79	14.4	80.0	570	10	US-10-301-480-493948 Sequence 493948, A
C 80	14.4	80.0	570	10	US-10-301-480-1107356 Sequence 1107356, A
C 81	14.4	80.0	570	10	US-10-301-480-1107357 Sequence 1107357, A
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C 84	14.4	80.0	579	6	US-09-925-065A-625667 Sequence 625667, A
C 85	14.4	80.0	579	10	US-10-301-480-1100823 Sequence 1100823, A
C 86	14.4	80.0	579	10	US-10-301-480-1100823 Sequence 1100823, A
C 87	14.4	80.0	584	6	US-09-925-065A-254371 Sequence 254371, A
C 88	14.4	80.0	584	6	US-09-925-065A-254372 Sequence 254372, A
C 89	14.4	80.0	584	9	US-10-301-480-69088 Sequence 69088, A
C 90	14.4	80.0	584	9	US-10-301-480-69089 Sequence 69089, A
C 91	14.4	80.0	584	10	US-10-301-480-682497 Sequence 682497, A

C 92	14.4	80.0	584	10	US-10-301-480-682498	Sequence 682498,	165	14	77.8	608	6	US-09-925-065A-862400	Sequence 862400,
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C 94	14.4	80.0	589	6	US-09-925-065A-73423	Sequence 73423, A	167	14	77.8	613	6	US-09-925-065A-873046	Sequence 873046,
C 95	14.4	80.0	589	6	US-09-925-065A-73424	Sequence 73424, A	168	14	77.8	623	6	US-09-925-065A-867206	Sequence 867206,
C 96	14.4	80.0	589	6	US-09-925-065A-73425	Sequence 73425, A	169	14	77.8	623	6	US-09-925-065A-867207	Sequence 867207,
C 97	14.4	80.0	589	6	US-10-301-480-174662	Sequence 174662,	170	14	77.8	640	6	US-09-925-065A-678311	Sequence 678311,
C 98	14.4	80.0	589	9	US-10-301-480-174663	Sequence 174663,	171	14	77.8	640	6	US-09-925-065A-678312	Sequence 678312,
C 99	14.4	80.0	589	9	US-10-301-480-174664	Sequence 174664,	172	14	77.8	640	6	US-09-925-065A-678313	Sequence 678313,
C 100	14.4	80.0	589	10	US-10-301-480-174664	Sequence 174664,	173	14	77.8	680	6	US-09-925-065A-709785	Sequence 709785,
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C 102	14.4	80.0	589	10	US-10-301-480-788073	Sequence 788073,	175	14	77.8	777	10	US-10-301-480-598834	Sequence 598834,
C 103	14.4	80.0	590	6	US-09-925-065A-951767	Sequence 951767,	176	14	77.8	1404	9	US-10-932-182A-79871	Sequence 79871, A
C 104	14.4	80.0	593	6	US-09-925-065A-109777	Sequence 109777,	177	14	77.8	1404	9	US-10-932-182A-79871	Sequence 79871, A
C 105	14.4	80.0	594	6	US-09-925-065A-819764	Sequence 819764,	178	14	77.8	1588	8	US-10-750-185-25515	Sequence 25515, A
C 106	14.4	80.0	594	6	US-09-925-065A-819765	Sequence 819765,	179	14	77.8	1588	8	US-10-750-185-25515	Sequence 25515, A
C 107	14.4	80.0	599	6	US-10-301-480-21094	Sequence 21094, A	180	14	77.8	2025	6	US-09-925-065A-94759	Sequence 94759, A
C 108	14.4	80.0	599	10	US-10-301-480-634503	Sequence 634503,	181	14	77.8	2025	6	US-09-925-065A-94760	Sequence 94760, A
C 109	14.4	80.0	600	10	US-10-301-480-518947	Sequence 518947,	182	14	77.8	2025	6	US-09-925-065A-94761	Sequence 94761, A
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C 113	14.4	80.0	601	10	US-10-301-480-946706	Sequence 946706,	186	14	77.8	2025	10	US-10-301-480-809411	Sequence 809411,
C 114	14.4	80.0	601	10	US-10-301-480-946707	Sequence 946707,	187	14	77.8	2025	10	US-10-301-480-809412	Sequence 809412,
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C 116	14.4	80.0	606	6	US-09-925-065A-431301	Sequence 431301,	189	14	77.8	156544	14	US-11-121-086-81	Sequence 81,
C 117	14.4	80.0	610	6	US-09-925-065A-462218	Sequence 462218,	190	14	77.8	241805	8	US-10-925-561-13215	Sequence 13215, A
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C 119	14.4	80.0	629	10	US-10-301-480-684452	Sequence 684452,	192	14	77.8	1082144	14	US-11-117-187-211	Sequence 211, Appl1
C 120	14.4	80.0	639	10	US-10-301-480-575387	Sequence 575387,	193	13.8	76.7	18	8	US-10-310-914A-381166	Sequence 381166,
C 121	14.4	80.0	639	10	US-10-301-480-1188796	Sequence 1188796,	194	13.8	76.7	25	9	US-10-932-182A-22217	Sequence 22217, A
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C 130	14.4	80.0	813	10	US-10-301-480-786976	Sequence 786976,	203	13.8	76.7	201	14	US-11-124-368A-18203	Sequence 18203, A
C 131	14.4	80.0	934	10	US-10-301-480-563017	Sequence 563017,	204	13.8	76.7	201	14	US-11-124-368A-18203	Sequence 18203, A
C 132	14.4	80.0	934	10	US-10-301-480-1196426	Sequence 1196426,	205	13.8	76.7	201	14	US-11-124-367A-22312	Sequence 22312, A
C 133	14.4	80.0	1262	6	US-09-925-065A-727391	Sequence 727391,	206	13.8	76.7	201	14	US-11-124-367A-2331	Sequence 2331, A
C 134	14.4	80.0	1262	6	US-09-925-065A-727392	Sequence 727392,	207	13.8	76.7	201	14	US-11-124-367A-2339	Sequence 2339, A
C 135	14.4	80.0	1262	6	US-09-925-065A-727393	Sequence 727393,	208	13.8	76.7	201	14	US-11-124-367A-2369	Sequence 2369, A
C 136	14.4	80.0	1322	8	US-10-750-185-41738	Sequence 41738, A	209	13.8	76.7	201	14	US-11-124-367A-2369	Sequence 2369, A
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C 140	14.4	80.0	1334	10	US-10-301-480-781620	Sequence 781620,	213	13.8	76.7	201	14	US-11-124-367A-15107	Sequence 15107, A
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C 154	14.4	80.0	515	6	US-09-925-065A-193359	Sequence 193359,	227	13.8	76.7	471	10	US-10-301-480-938830	Sequence 938830,
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C 157	14.4	80.0	520	10	US-10-301-480-840973	Sequence 840973,	230	13.8	76.7	483	10	US-10-301-480-672333	Sequence 672333,
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ALIGNMENTS

RESULT 1
US-10-301-480-55145
; Sequence 55145, Application US/10301480
; Publication No. US2006005564A1
; GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55145
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-55145

Query Match 85.6%; Score 15.4; DB 9; Length 539;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 GGACCTAGAGGCAAG 18
Db 63 GGACCTGGAGGCAAG 79

RESULT 2
US-10-301-480-668554
; Sequence 668554, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 668554
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-668554

Query Match 85.6%; Score 15.4; DB 10; Length 539;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 GGACCTAGAGGCAAG 18
Db 63 GGACCTGGAGGCAAG 79

RESULT 3
US-09-925-065A-504327/c
; Sequence 504327, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147


```

; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 504327
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-504327
```

```

Query Match      85.6%; Score 15.4; DB 6; Length 574;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 GGACCTTAGAGGCAAG 18
      |||||
DB      361 GGACCCCAAGGCAAG 345
```

```

RESULT 4
US-09-925-065A-65294/c
; Sequence 65294, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65294
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-65294
```

```

Query Match      85.6%; Score 15.4; DB 6; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 GGACCTTAGAGGCAAG 18
      |||||
DB      498 GGACCTTAGAGGCAAG 482
```

```

RESULT 5
US-09-925-065A-65295/c
; Sequence 65295, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
```

```

; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65295
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-65295
```

```

Query Match      85.6%; Score 15.4; DB 6; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 GGACCTTAGAGGCAAG 18
      |||||
DB      498 GGACCTTAGAGGCAAG 482
```

```

RESULT 6
US-09-925-065A-65296/c
; Sequence 65296, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65296
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-65296
```

```

Query Match      85.6%; Score 15.4; DB 6; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 GGACCTTAGAGGCAAG 18
      |||||
DB      498 GGACCTTAGAGGCAAG 482
```

```

RESULT 7
US-10-301-480-165533/c
; Sequence 16533, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
```

FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 166533
LENGTH: 738
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-166533

Query Match 85.6%; Score 15.4; DB 9; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTTAGAGGCAAG 18
Db 498 GGACCTTAGAGGCAAG 482

RESULT 8
US-10-301-480-166534/c
Sequence 166534, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 166534
LENGTH: 738
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-166534

Query Match 85.6%; Score 15.4; DB 9; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTTAGAGGCAAG 18
Db 498 GGACCTTAGAGGCAAG 482

RESULT 9
US-10-301-480-166535/c
Sequence 166535, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 166535
LENGTH: 738
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-166535

Query Match 85.6%; Score 15.4; DB 9; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTTAGAGGCAAG 18
Db 498 GGACCTTAGAGGCAAG 482

RESULT 10
US-10-301-480-779942/c
Sequence 779942, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 779942
LENGTH: 738
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-779942

Query Match 85.6%; Score 15.4; DB 10; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTTAGAGGCAAG 18
Db 498 GGACCTTAGAGGCAAG 482

RESULT 11
US-10-301-480-779943/c
Sequence 779943, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 779943
LENGTH: 738
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-779943

Query Match 85.6%; Score 15.4; DB 10; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGCAAG 18
|||
DB 498 GGACCTAGAGCAAG 482

RESULT 12
US-10-301-480-779944/c
; Sequence 779944, Application US/10301480
; Publication No. US2006005754A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 779944
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-779944

Query Match 85.6%; Score 15.4; DB 10; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGCAAG 18
|||
DB 498 GGACCTAGAGCAAG 482

RESULT 13
US-10-750-185-61166
; Sequence 61166, Application US/10750185
; Publication No. US20050280603A1
; GENERAL INFORMATION:
; APPLICANT: MWI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61166
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Bovine 19866881037774
US-10-750-185-61166

Query Match 85.6%; Score 15.4; DB 8; Length 1155;
Best Local Similarity 94.1%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGCAAG 18
|||
DB 869 GGACCTAGAGCAAG 885

RESULT 14
US-10-750-623-61166
; Sequence 61166, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MWI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61166
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Bovine 19866881037774
US-10-750-623-61166

Query Match 85.6%; Score 15.4; DB 8; Length 1155;
Best Local Similarity 94.1%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGCAAG 18
|||
DB 869 GGACCTAGAGCAAG 885

RESULT 15
US-10-932-182A-2596/c
; Sequence 2596, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, YOSHIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2596
; LENGTH: 1206
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2596

Query Match 85.6%; Score 15.4; DB 9; Length 1206;
Best Local Similarity 94.1%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGACCTAGAGCAAA 17
|||
DB 1141 GGACCTAGAGCAAA 1125

RESULT 16
US-10-932-182A-2596/c
; Sequence 2596, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA

APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 2596
LENGTH: 1206
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2596

Query Match 85.6%; Score 15.4; DB 9; Length 1206;
Best Local Similarity 94.1%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGACCTTAGGCGCAA 17
Db 1141 CGGACCTTAGGCGCAA 1125

RESULT 17
US-11-096-568A-33576/c
Sequence 33576, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PU52
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 33576
LENGTH: 1806
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)-(1806)
OTHER INFORMATION: Ceres Seq. ID no. 13603467
US-11-096-568A-33576

Query Match 85.6%; Score 15.4; DB 11; Length 1806;
Best Local Similarity 94.1%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTTAGGCGCAA 18
Db 915 GGACCTTAGGCGCAATG 899

RESULT 18
US-11-096-568A-2408/c
Sequence 2408, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PU52
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 2408
LENGTH: 1862
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature

LOCATION: (1)-(1862)
OTHER INFORMATION: Ceres Seq. ID no. 14312112
US-11-096-568A-2408

Query Match 85.6%; Score 15.4; DB 11; Length 1862;
Best Local Similarity 94.1%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTTAGGCGCAA 18
Db 948 GGACCTTAGGCGCAATG 932

RESULT 19
US-11-128-061-856/c
Sequence 856, Application US/11128061
Publication No. US2006003958A1
GENERAL INFORMATION:
APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane E.
APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
FILE REFERENCE: 01997,027701
CURRENT APPLICATION NUMBER: US/11/128,061
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
SEQ ID NO 856
LENGTH: 8703
TYPE: DNA
ORGANISM: Mesocricetus auratus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (279)-(291)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (293)-(321)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (331)-(349)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (402)-(414)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (417)-(446)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1384)-(1455)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1728)-(1776)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2778)-(2795)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature

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LOCATION: (3235)..(3257)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (3287)..(3340)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (3342)..(3362)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (4001)..(4025)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (4437)..(4454)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (4895)..(4922)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (7677)..(7701)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (7861)..(7903)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (7932)..(7949)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (8381)..(8418)
OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-856
```

```
Query Match 85.6%; Score 15.4; DB 14; Length 8703;
Best Local Similarity 94.1%; Pred.No.3.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 2 GGACCTAGAGCAAG 18
DB 6031 GGACCTAGAGCAAG 6015
```

```
RESULT 20
US-11-128-049-856/c
Sequence 856, Application US/11128049
Publication No. US20060010513A1
GENERAL INFORMATION:
APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane E.
APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
FILE REFERENCE: 01997.027700
CURRENT APPLICATION NUMBER: US/11/128,049
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
SEQ ID NO 856
LENGTH: 8703
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TYPE: DNA
ORGANISM: Mesocricetus auratus
FEATURE:
NAME/KEY: misc feature
LOCATION: (279)..(291)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (293)..(321)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (331)..(349)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (402)..(414)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (417)..(446)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1384)..(1455)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1728)..(1776)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (2778)..(2795)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (3235)..(3257)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (3287)..(3340)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (3342)..(3362)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (4001)..(4025)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (4437)..(4454)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (4895)..(4922)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (7677)..(7701)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (7861)..(7903)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (7932)..(7949)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (8381)..(8418)
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OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-856

Query Match 85.6%; Score 15.4; DB 14; Length 8703;
Best Local Similarity 94.1%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAAG 18
Db 6031 GGACCTTAGAGGCAAG 6015

RESULT 21

US-10-330-773-975/c
Sequence 975, Application US/10330773
Publication No. US20060040262a1
GENERAL INFORMATION:
APPLICANT: David W. Morris
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 975
LENGTH: 22475
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1)...(22475)
OTHER INFORMATION: n = A,T,C or G
US-10-330-773-975

Query Match 85.6%; Score 15.4; DB 9; Length 22475;
Best Local Similarity 94.1%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAAG 18
Db 15390 GGACCTTAGAGGCAAG 15374

RESULT 22

US-11-124-367A-5024
Sequence 5024, Application US/11124367A
Publication No. US20060024700A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CU001519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5024
LENGTH: 100000
TYPE: DNA
ORGANISM: Homo sapiens
US-11-124-367A-5024

Query Match 85.6%; Score 15.4; DB 14; Length 100000;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAAG 18
Db 27957 GGACCTTAGAGGCAAG 27973

RESULT 23

US-11-121-086-98/c
Sequence 98, Application US/1121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 98
LENGTH: 171732
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-086-98

Query Match 85.6%; Score 15.4; DB 14; Length 171732;
Best Local Similarity 94.1%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAAG 18
Db 12979 GGACCTTAGAGGCAAG 12963

RESULT 24

US-11-101-244-1292346
Sequence 1292346, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Pharmacia, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1292346
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1292346

Query Match 83.3%; Score 15; DB 12; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCA 16
Db 4 GGACCTTAGAGGCA 18

RESULT 25

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US-11-101-244-1292367
; Sequence 1292367, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1292367
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1292367
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Query Match
Best Local Similarity 83.3%; Score 15; DB 12; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY 2 GGACCTAGAGGCAA 16
DB 1 GGACCTAGAGGCAA 15
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RESULT 26
US-11-083-784-1292346
; Sequence 1292346, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1292346
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1292346
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Query Match
Best Local Similarity 83.3%; Score 15; DB 13; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
OY 2 GGACCTAGAGGCAA 16
DB 4 GGACCTAGAGGCAA 18
```

```
RESULT 27
US-11-083-784-1292367
; Sequence 1292367, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1292367
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1292367
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Query Match
Best Local Similarity 83.3%; Score 15; DB 13; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY 2 GGACCTAGAGGCAA 16
DB 1 GGACCTAGAGGCAA 15
```

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RESULT 28
US-10-310-914A-965984/c
; Sequence 965984, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Yvzatz
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087,0200,CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 965984
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-965984
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Query Match
Best Local Similarity 83.3%; Score 15; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 2 GGACCTAGAGGCAA 16
DB 17 GGACCTAGAGGCAA 3
```

```
RESULT 29
US-09-925-065A-799050/c
; Sequence 799050, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

```

; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 799050
; LENGTH: 640
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-799050
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Query Match      83.3%; Score 15; DB 6; Length 640;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      2 GGACCTAGAGCAA 16
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Db      580 GGACCTAGAGCAA 566
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RESULT 30
US-09-925-065A-799051/C
; Sequence 799051, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 799051
; LENGTH: 640
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-799051
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Query Match      83.3%; Score 15; DB 6; Length 640;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      2 GGACCTAGAGCAA 16
      |||||
Db      580 GGACCTAGAGCAA 566
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Search completed: April 15, 2006, 18:19:53
Job time : 425 secs
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 18:09:33 ; Search time 806 Seconds
(without alignments)
184.676 Million cell updates/sec

Title: US-10-727-358-5

Perfect score: 18

Sequence: 1 cggaccctagaggaag 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications NA Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	US-10-727-358-5	Sequence 5, Appl1
2	18	100.0	18	US-10-727-358-15	Sequence 15, Appl1
3	18	100.0	18	US-10-727-358-28	Sequence 28, Appl1
4	18	100.0	25	US-11-036-317-881396	Sequence 881396, Appl1
5	18	100.0	25	US-11-036-317-904638	Sequence 904638, Appl1
6	18	100.0	25	US-11-036-317-910916	Sequence 910916, Appl1
7	18	100.0	120	US-10-727-358-1	Sequence 1, Appl1
8	18	100.0	121	US-10-727-358-25	Sequence 25, Appl1
9	18	100.0	2601	US-10-727-358-24	Sequence 24, Appl1
10	18	100.0	2632	US-10-085-117-33	Sequence 33, Appl1
11	18	100.0	4034	US-10-085-117-32	Sequence 32, Appl1
12	18	100.0	4094	US-10-727-358-11	Sequence 11, Appl1
13	16.4	91.1	25	US-11-036-317-881395	Sequence 881395, Appl1
14	16.4	91.1	25	US-11-036-317-904637	Sequence 904637, Appl1
15	16.4	91.1	25	US-11-036-317-910915	Sequence 910915, Appl1
16	16	88.9	16	US-10-727-358-8	Sequence 8, Appl1
17	16	88.9	25	US-11-036-317-928166	Sequence 928166, Appl1
18	15.4	85.6	233	US-10-242-535A-12378	Sequence 12378, A
19	15.4	85.6	233	US-10-085-783A-12378	Sequence 12378, A
20	15.4	85.6	376	US-09-964-824A-522	Sequence 522, App
21	15.4	85.6	376	US-09-969-708-67	Sequence 67, Appl1
22	15.4	85.6	376	US-10-843-641A-5825	Sequence 5825, App
23	15.4	85.6	376	US-10-843-641A-7538	Sequence 7538, App

24	15.4	85.6	283	US-10-425-115-110504	Sequence 110504, Appl1
25	15.4	85.6	481	US-10-027-632-141547	Sequence 141547, Appl1
26	15.4	85.6	481	US-10-027-632-141547	Sequence 141547, Appl1
27	15.4	85.6	514	US-09-764-872-162	Sequence 162, App
28	15.4	85.6	546	US-10-027-632-202268	Sequence 202268, Appl1
29	15.4	85.6	546	US-10-027-632-202268	Sequence 202268, Appl1
30	15.4	85.6	547	US-10-424-599-52757	Sequence 52757, A
31	15.4	85.6	574	US-09-925-065A-504327	Sequence 504327, Appl1
32	15.4	85.6	611	US-10-027-632-228051	Sequence 228051, Appl1
33	15.4	85.6	611	US-10-027-632-228051	Sequence 228051, Appl1
34	15.4	85.6	738	US-09-925-065A-65294	Sequence 65294, A
35	15.4	85.6	738	US-09-925-065A-65295	Sequence 65295, A
36	15.4	85.6	738	US-09-925-065A-65296	Sequence 65296, A
37	15.4	85.6	751	US-10-027-632-19033	Sequence 19033, A
38	15.4	85.6	751	US-10-027-632-19033	Sequence 19033, A
39	15.4	85.6	1797	US-10-723-860-7641	Sequence 7641, App
40	15.4	85.6	9645	US-10-723-860-896	Sequence 896, App
41	15.4	85.6	9645	US-10-756-149-895	Sequence 895, App
42	15.4	85.6	314364	US-10-917-647-3	Sequence 3, Appl1
43	15	83.3	50	US-10-131-827-7589	Sequence 7589, App
44	15	83.3	75	US-10-466-894-1339	Sequence 1339, App
45	15	83.3	265	US-10-242-535A-13707	Sequence 13707, A
46	15	83.3	265	US-10-085-783A-13707	Sequence 13707, A
47	15	83.3	285	US-10-424-599-34328	Sequence 34328, A
48	15	83.3	320	US-10-242-535A-6362	Sequence 6362, App
49	15	83.3	320	US-10-085-783A-6362	Sequence 6362, App
50	15	83.3	327	US-10-242-535A-13737	Sequence 13737, App
51	15	83.3	327	US-10-085-783A-13737	Sequence 13737, A
52	15	83.3	342	US-09-878-170-1986	Sequence 1986, App
53	15	83.3	342	US-10-046-935-1986	Sequence 1986, App
54	15	83.3	342	US-10-146-502-1996	Sequence 1996, App
55	15	83.3	412	US-09-918-995-37155	Sequence 37155, App
56	15	83.3	444	US-09-822-846-548	Sequence 548, App
57	15	83.3	478	US-09-918-995-16549	Sequence 16549, A
58	15	83.3	554	US-10-091-504-334	Sequence 334, App
59	15	83.3	554	US-10-027-577-334	Sequence 334, App
60	15	83.3	554	US-10-027-632-282238	Sequence 282238, Appl1
61	15	83.3	576	US-10-027-632-282238	Sequence 282238, Appl1
62	15	83.3	576	US-10-027-632-309560	Sequence 309560, Appl1
63	15	83.3	600	US-10-956-157-7765	Sequence 7765, App
64	15	83.3	606	US-10-027-632-309560	Sequence 309560, Appl1
65	15	83.3	606	US-10-027-632-309560	Sequence 309560, Appl1
66	15	83.3	606	US-10-027-632-309560	Sequence 309560, Appl1
67	15	83.3	606	US-10-027-632-309560	Sequence 309560, Appl1
68	15	83.3	627	US-09-971-392-213	Sequence 213, App
69	15	83.3	640	US-09-925-065A-799051	Sequence 799051, Appl1
70	15	83.3	640	US-09-925-065A-799051	Sequence 799051, Appl1
71	15	83.3	640	US-09-925-065A-799051	Sequence 799051, Appl1
72	15	83.3	640	US-09-925-065A-799051	Sequence 799051, Appl1
73	15	83.3	669	US-09-925-065A-799051	Sequence 799051, Appl1
74	15	83.3	669	US-09-925-065A-799051	Sequence 799051, Appl1
75	15	83.3	764	US-10-956-157-2530	Sequence 2530, App
76	15	83.3	779	US-09-822-846-549	Sequence 549, App
77	15	83.3	782	US-09-822-846-549	Sequence 549, App
78	15	83.3	2278	US-10-108-260A-62	Sequence 62, Appl1
79	15	83.3	2399	US-10-641-643-508	Sequence 508, App
80	15	83.3	5760	US-11-097-143-33785	Sequence 33785, App
81	15	83.3	44449	US-10-087-129-280	Sequence 280, App
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ALIGNMENTS

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; Publication No. US20050037455A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: King, Hong-Mei R.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED
; TITLE OF INVENTION: TUMORIGENESIS

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; FILE REFERENCE: 1216-1-006CIP
; CURRENT APPLICATION NUMBER: US/10/727,358
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/384,228
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/460,023
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: PCT/US03/16961
; PRIOR FILING DATE: 2003-05-29
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; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: King, Hong-Mei R.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED
; TITLE OF INVENTION: TUMORIGENESIS
; FILE REFERENCE: 1216-1-006CIP
; CURRENT APPLICATION NUMBER: US/10/727,358
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; APPLICANT: Kolesnick, Richard N.
; APPLICANT: King, Hong-Mei R.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED
; TITLE OF INVENTION: TUMORIGENESIS

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;; TITLE OF INVENTION: TUMORIGENESIS
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Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGACCTTAGAGGCAAG 18
Db 18 CGGACCTTAGAGGCAAG 1

RESULT 4
US-11-036-317-881396
;; Sequence 881396, Application US/11036317
;; Publication No. US20050214823A1
;; GENERAL INFORMATION:
;; APPLICANT: Williams, Alan
;; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;; FILE REFERENCE: 3654.1
;; CURRENT APPLICATION NUMBER: US/11/036,317
;; CURRENT FILING DATE: 2005-01-13
;; PRIOR APPLICATION NUMBER: US 60/536,639
;; PRIOR FILING DATE: 2004-01-13
;; NUMBER OF SEQ ID NOS: 991174
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 881396
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-11-036-317-881396

Query Match 100.0%; Score 18; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGACCTTAGAGGCAAG 18
Db 4 CGGACCTTAGAGGCAAG 21

RESULT 5
US-11-036-317-904638
;; Sequence 904638, Application US/11036317
;; Publication No. US20050214823A1
;; GENERAL INFORMATION:
;; APPLICANT: Williams, Alan
;; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;; FILE REFERENCE: 3654.1
;; CURRENT APPLICATION NUMBER: US/11/036,317
;; CURRENT FILING DATE: 2005-01-13
;; PRIOR APPLICATION NUMBER: US 60/536,639
;; PRIOR FILING DATE: 2004-01-13
;; NUMBER OF SEQ ID NOS: 991174

;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 904638
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-11-036-317-904638

Query Match 100.0%; Score 18; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGACCTTAGAGGCAAG 18
Db 2 CGGACCTTAGAGGCAAG 19

RESULT 6
US-11-036-317-910916
;; Sequence 910916, Application US/11036317
;; Publication No. US20050214823A1
;; GENERAL INFORMATION:
;; APPLICANT: Williams, Alan
;; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;; FILE REFERENCE: 3654.1
;; CURRENT APPLICATION NUMBER: US/11/036,317
;; CURRENT FILING DATE: 2005-01-13
;; PRIOR APPLICATION NUMBER: US 60/536,639
;; PRIOR FILING DATE: 2004-01-13
;; NUMBER OF SEQ ID NOS: 991174
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 910916
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-11-036-317-910916

Query Match 100.0%; Score 18; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGACCTTAGAGGCAAG 18
Db 1 CGGACCTTAGAGGCAAG 18

RESULT 7
US-10-727-358-1
;; Sequence 1, Application US/10727358
;; Publication No. US20050037455A1
;; GENERAL INFORMATION:
;; APPLICANT: Memorial Sloan-Kettering Cancer Center
;; APPLICANT: Kolesnick, Richard N.
;; APPLICANT: Xing, Hong-Mei R.
;; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDiate
;; FILE REFERENCE: 1216-1-006CIP
;; CURRENT APPLICATION NUMBER: US/10/727,358
;; CURRENT FILING DATE: 2003-12-03
;; PRIOR APPLICATION NUMBER: 60/384,228
;; PRIOR FILING DATE: 2002-05-30
;; PRIOR APPLICATION NUMBER: 60/460,023
;; PRIOR FILING DATE: 2003-04-03
;; PRIOR APPLICATION NUMBER: PCT/US03/16961
;; PRIOR FILING DATE: 2003-05-29
;; NUMBER OF SEQ ID NOS: 38
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 1
;; LENGTH: 120
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-727-358-1

Query Match 100.0%; Score 18; DB 8; Length 120;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGACCTAGAGGCAAG 18
|||
Db 91 CGGACCTAGAGGCAAG 108

RESULT 8
US-10-727-358-25
; Sequence 25, Application US/10727358
; Publication No. US20050037455A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: Xing, Hong-Mei R.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED
; TITLE OF INVENTION: TUMORIGENESIS
; FILE REFERENCE: 1216-1-006CIP
; CURRENT APPLICATION NUMBER: US/10/727,358
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/384,228
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/460,023
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: PCT/US03/16961
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-727-358-25

Query Match 100.0%; Score 18; DB 8; Length 121;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18
|||
Db 91 CGGACCTAGAGGCAAG 108

RESULT 9
US-10-727-358-24
; Sequence 24, Application US/10727358
; Publication No. US20050037455A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: Xing, Hong-Mei R.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED
; TITLE OF INVENTION: TUMORIGENESIS
; FILE REFERENCE: 1216-1-006CIP
; CURRENT APPLICATION NUMBER: US/10/727,358
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/384,228
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/460,023
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: PCT/US03/16961
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 2601
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-727-358-24

Query Match 100.0%; Score 18; DB 8; Length 2601;

Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGACCTAGAGGCAAG 18
|||
Db 187 CGGACCTAGAGGCAAG 204

RESULT 10
US-10-085-117-33
; Sequence 33, Application US/10085117
; Publication No. US2003023334A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2622
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-085-117-33

Query Match 100.0%; Score 18; DB 6; Length 2622;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18
|||
Db 214 CGGACCTAGAGGCAAG 231

RESULT 11
US-10-085-117-32
; Sequence 32, Application US/10085117
; Publication No. US2003023334A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 4094
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-085-117-32

Query Match 100.0%; Score 18; DB 6; Length 4094;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18
|||
Db 296 CGGACCTAGAGGCAAG 313

RESULT 12
US-10-727-358-11
; Sequence 11, Application US/10727358
; Publication No. US20050037455A1
; GENERAL INFORMATION:

```

; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: Xing, Hong-Mei R.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED
; TITLE OF INVENTION: TUMORIGENESIS
; FILE REFERENCE: 1216-1-006CIP
; CURRENT APPLICATION NUMBER: US/10/727,358
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/384,228
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/460,023
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: PCT/US03/16961
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 4094
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-727-358-11

Query Match      100.0%; Score 18; DB 8; Length 4094;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGACCTTAGAGGCAAG 18
      |||
Db      296 CGGACCTTAGAGGCAAG 313

RESULT 13
US-11-036-317-881395
; Sequence 881395, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 881395
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-881395

Query Match      91.1%; Score 16.4; DB 10; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGGACCTTAGAGGCAAG 18
      |||
Db      4 CGGACCTTAGAGGCAAG 21

RESULT 14
US-11-036-317-904637
; Sequence 904637, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
```

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; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 904637
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-904637

Query Match      91.1%; Score 16.4; DB 10; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGGACCTTAGAGGCAAG 18
      |||
Db      2 CGGACCTTAGAGGCAAG 19

RESULT 15
US-11-036-317-910915
; Sequence 910915, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 910915
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-910915

Query Match      91.1%; Score 16.4; DB 10; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGGACCTTAGAGGCAAG 18
      |||
Db      1 CGGACCTTAGAGGCAAG 18

RESULT 16
US-10-727-358-8/c
; Sequence 8, Application US/10727358
; Publication No. US20050037455A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: Xing, Hong-Mei R.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATE
; TITLE OF INVENTION: TUMORIGENESIS
; FILE REFERENCE: 1216-1-006CIP
; CURRENT APPLICATION NUMBER: US/10/727,358
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/384,228
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/460,023
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: PCT/US03/16961
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
FEATURE:
OTHER INFORMATION: antisense oligonucleotide
US-10-727-358-8

Query Match      88.9%; Score 16; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GACCTAGAGGCAAG 18
      |||||
      16 GACCTAGAGGCAAG 1

RESULT 17
US-11-036-317-928166
Sequence 928166, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
PRIOR FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 928166
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-928166

Query Match      88.9%; Score 16; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GACCTAGAGGCAAG 18
      |||||
      1 GACCTAGAGGCAAG 16

Db

RESULT 18
US-10-242-535A-12378/c
Sequence 12378, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12378
LENGTH: 233
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (13)-(13)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
```

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NAME/KEY: misc_feature
LOCATION: (28)-(28)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (34)-(34)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (39)-(39)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (66)-(66)
OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-12378

Query Match      85.6%; Score 15.4; DB 7; Length 233;
Best Local Similarity 94.1%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGACCTAGAGGCAAG 18
      |||||
      188 GGACCTAGAGGCAAG 172

Db

RESULT 19
US-10-085-783A-12378/c
Sequence 12378, Application US/10085783A
Publication No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12378
LENGTH: 233
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (13)-(13)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (28)-(28)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (34)-(34)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (39)-(39)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (66)-(66)
OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-12378

Query Match      85.6%; Score 15.4; DB 7; Length 233;
Best Local Similarity 94.1%; Pred. No. 4.6e+02;
```

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTAGAGGCAAG 18
Db 188 GGACCTAGAGGCAAG 172

RESULT 20
US-09-964-824A-522/c
; Sequence 522, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 522
; LENGTH: 376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-522

Query Match 85.6%; Score 15.4; DB 3; Length 376;
Best Local Similarity 94.1%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTAGAGGCAAG 18
Db 107 GGACCTAGAGGCAAG 91

RESULT 21
US-09-969-708-67/c
; Sequence 67, Application US/09969708
; Patent No. US20020102532A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature
; FILE REFERENCE: 689290-70
; CURRENT APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: US/60/237,606
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,608
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,425
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-708-67

Query Match 85.6%; Score 15.4; DB 3; Length 376;
Best Local Similarity 94.1%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTAGAGGCAAG 18
Db 107 GGACCTAGAGGCAAG 91

RESULT 22
US-10-843-641A-5825/c
; Sequence 5825, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5825
; LENGTH: 376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-5825

Query Match 85.6%; Score 15.4; DB 9; Length 376;
Best Local Similarity 94.1%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTAGAGGCAAG 18
Db 107 GGACCTAGAGGCAAG 91

RESULT 23
US-10-843-641A-7538/c
; Sequence 7538, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824

PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/09/967,768
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/968,007
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/969,347
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/969,708
PRIOR FILING DATE: 2001-10-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 8447
SOFTWARE: Patentin version 3.0
SEQ ID NO 7538
LENGTH: 376
TYPE: DNA
ORGANISM: Homo sapiens
US-10-843-641A-7538

Query Match 85.6%; Score 15.4; DB 9; Length 376;
Best Local Similarity 94.1%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18
DB 107 GGACCTAGAGGCAAG 91

RESULT 24
US-10-425-115-110504
Sequence 110504, Application US/10425115
Publication No. US2004021272M1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 110504
LENGTH: 383
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MFT4577_32272C.1
US-10-425-115-110504

Query Match 85.6%; Score 15.4; DB 8; Length 383;
Best Local Similarity 94.1%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18
DB 3 GGACCTAGAGGCAAG 19

RESULT 25
US-10-027-632-141547
Sequence 141547, Application US/10027632
Publication No. US2002019837A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 141547
LENGTH: 481
TYPE: DNA
ORGANISM: Human
US-10-027-632-141547

Query Match 85.6%; Score 15.4; DB 5; Length 481;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18
DB 255 GGACCTAGAGGCAAG 271

RESULT 26
US-10-027-632-141547
Sequence 141547, Application US/10027632
Publication No. US20030204075A9

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 141547
LENGTH: 481
TYPE: DNA
ORGANISM: Human
US-10-027-632-141547

Query Match 85.6%; Score 15.4; DB 6; Length 481;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18
DB 255 GGACCTAGAGGCAAG 271

RESULT 27
US-09-764-872-162/C
Sequence 162, Application US/09764872

Publication No. US20030050231A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA125
CURRENT APPLICATION NUMBER: US/09/764,872
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 957
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 162
LENGTH: 514
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-872-162

Query Match 85.6%; Score 15.4; DB 3; Length 514;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18
DB 430 GGACCTAGAGGCCAAG 414

RESULT 28
US-10-027-632-202268
Sequence 202268, Application US/10027632
Publication No. US2002019871A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 202268
LENGTH: 546
TYPE: DNA
ORGANISM: Human
US-10-027-632-202268

Query Match 85.6%; Score 15.4; DB 5; Length 546;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18
DB 62 GGACCTAGAGGCAAG 78

RESULT 29
US-10-027-632-202268
Sequence 202268, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 202268
LENGTH: 546
TYPE: DNA
ORGANISM: Human
US-10-027-632-202268

Query Match 85.6%; Score 15.4; DB 6; Length 546;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18
DB 62 GGACCTAGAGGCAAG 78

RESULT 30
US-10-424-599-52757
Sequence 52757, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovacic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 52757
LENGTH: 547
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_18652C.1
US-10-424-599-52757

Query Match 85.6%; Score 15.4; DB 7; Length 547;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18
DB 366 GGACCTAGAGGCAAG 382

Search completed: April 16, 2006, 01:39:37
Job time : 819 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 17:47:14 ; Search time 3806 Seconds
(without alignments)
221.274 Million cell updates/sec

Title: US-10-727-358-5

Perfect score: 18

Sequence: 1 cggaccctagagcgaag 18

Scoring table: IDENTITY NUC
Gapop 10-0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 300 summaries

Database :

EST.*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	656	2	BB629501 BB629501
2	18	100.0	674	5	BY727643 BY727643
3	18	100.0	668	2	BB613725 BB613725
4	18	100.0	2751	4	AK036566 Mus muscu
5	16.4	91.1	317	7	CK370327 zmtw005
6	16.4	91.1	370	6	CF633642 zmtw000
7	16.4	91.1	510	2	BE717998 PM1-HT079
8	16.4	91.1	704	10	AG354283 Mus muscu
9	16.4	91.1	744	8	DT058958 AGENCOURT
10	16.4	91.1	817	8	CX910994 UGI-CAN2
11	16.4	91.1	875	8	DT058819 AGENCOURT
12	16.4	88.9	296	2	BB247762 BB247762
13	16.4	88.9	396	2	BE768604 OY2-FT001
14	16.4	88.9	430	1	AT762325 W97A04.x
15	16.4	88.9	507	1	BM029828 A8200.MA
16	16.4	88.9	538	1	AT208178 G955a08.x
17	16.4	88.9	769	10	AG498153 Mus muscu
18	15.4	85.6	123	2	BE503972 h254a03.x
19	15.4	85.6	143	1	AI349272 ta75c07.x
20	15.4	85.6	170	1	AA654607 nt59e02.8
21	15.4	85.6	177	1	AA234751 z838c05.8
22	15.4	85.6	205	1	AI099443 uc30106.x

23	15.4	85.6	215	3	BI493189
24	15.4	85.6	241	9	BH084942
25	15.4	85.6	258	3	BI493190
26	15.4	85.6	288	2	BG384534 303762.MA
27	15.4	85.6	295	1	AA746945 nx62h05.s
28	15.4	85.6	296	1	AA747067 nx65d11.s
29	15.4	85.6	313	1	AM087244 xp97c11.x
30	15.4	85.6	326	3	BM743266 K-EST0016
31	15.4	85.6	336	9	AZ801445 2M0059122
32	15.4	85.6	338	8	DN150252 5238.H01
33	15.4	85.6	348	5	BU680671 UI-CF-DU1
34	15.4	85.6	350	1	AI678934 tc99c04.x
35	15.4	85.6	351	9	AZ430853 1M0215B04
36	15.4	85.6	353	10	AG589928 Mus muscu
37	15.4	85.6	364	7	CV310713 CM0-FT004
38	15.4	85.6	376	1	AA598484 ae38f04.s
39	15.4	85.6	377	5	BQ497250 EST06479
40	15.4	85.6	387	1	AM013825 UI-H-B10
41	15.4	85.6	389	8	W60314 zd29f02.81
42	15.4	85.6	392	1	AI719432 ae64e10.x
43	15.4	85.6	392	3	BM504405 lh22e03.y
44	15.4	85.6	392	3	BM746356 K-EST0020
45	15.4	85.6	393	1	AM301584 xp98b04.x
46	15.4	85.6	393	3	BM929646 UI-E-EJ1-
47	15.4	85.6	397	1	AM392370 NR4-ST024
48	15.4	85.6	397	3	BM683597 UI-E-EJ1-
49	15.4	85.6	399	2	BF109890 7170h03.x
50	15.4	85.6	402	1	AI948978 wg17g06.x
51	15.4	85.6	407	2	BI120589 F018P82Y
52	15.4	85.6	410	2	AA977744 OG48812.s
53	15.4	85.6	413	2	BE670735 7g40e05.x
54	15.4	85.6	413	3	BM504184 ih22e03.x
55	15.4	85.6	416	1	AV759284 AV759284
56	15.4	85.6	428	2	BF445861 7p38c12.x
57	15.4	85.6	429	1	AM891826 CM3-N7008
58	15.4	85.6	429	2	BF195828 7g82g08.x
59	15.4	85.6	431	2	BF110503 7h38c05.x
60	15.4	85.6	436	1	BM673461 1aa12a09.
61	15.4	85.6	442	7	CN310816 170006001
62	15.4	85.6	448	1	AI698018 we19h08.x
63	15.4	85.6	449	1	AL537377 AL537377
64	15.4	85.6	451	1	AA235149 z683c05.x
65	15.4	85.6	458	1	AA781074 aj23808.s
66	15.4	85.6	460	1	AA004425 znh7d06.8
67	15.4	85.6	472	2	BG700645 602682256
68	15.4	85.6	475	1	AL537378 AL537378
69	15.4	85.6	476	6	CA866752 1r72a07.x
70	15.4	85.6	479	4	CR614418 full1-1eng
71	15.4	85.6	488	3	BM930208 UI-E-EJ1-
72	15.4	85.6	489	3	BM683685 UI-E-EJ1-
73	15.4	85.6	490	6	CD237050 FNPACB03
74	15.4	85.6	491	1	AV756616 AV756616
75	15.4	85.6	494	10	CG850061 ZMBB0303
76	15.4	85.6	497	3	CC549348 CH240.433
77	15.4	85.6	498	3	BQ278252 AGENCOURT
78	15.4	85.6	499	3	BM507041 ih24a11.y
79	15.4	85.6	504	6	CB961454 AGENCOURT
80	15.4	85.6	504	6	CB991682 AGENCOURT
81	15.4	85.6	504	6	CB991682 AGENCOURT
82	15.4	85.6	504	6	CD110174 AGENCOURT
83	15.4	85.6	517	2	BG528700 602579593
84	15.4	85.6	517	2	BM746988 K-EST0021
85	15.4	85.6	518	9	AO412745 RPCI-11-1
86	15.4	85.6	523	9	AO38717 RPCI-11-3
87	15.4	85.6	525	3	BM845464 K-EST0123
88	15.4	85.6	526	9	AZ065485 RPCI-23-4
89	15.4	85.6	529	8	CX593974 CT020007A
90	15.4	85.6	542	3	BM822753 K-EST0092
91	15.4	85.6	543	2	BF732540 nae12a11.
92	15.4	85.6	547	3	BI787490 sa146c11.
93	15.4	85.6	553	5	BU137811 603124903
94	15.4	85.6	559	3	BM822827 K-EST0093
95	15.4	85.6	561	9	AZ392033 1M0154P21

C 96	15.4	85.6	572	10	CE785184	C 169	15	83.3	175	1	AA151954
C 97	15.4	85.6	573	9	BZ539545	C 170	15	83.3	179	1	AA559544
C 98	15.4	85.6	574	7	CK905522	C 171	15	83.3	180	2	BI005692
C 99	15.4	85.6	577	9	AZ591114	C 172	15	83.3	182	1	AA481544
C 100	15.4	85.6	579	9	BZ539539	C 173	15	83.3	185	5	BU670987
C 101	15.4	85.6	579	11	CR116258	C 174	15	83.3	193	1	AA853831
C 102	15.4	85.6	580	5	BW148814	C 175	15	83.3	194	2	EG035839
C 103	15.4	85.6	596	9	AQ918955	C 176	15	83.3	201	1	AI1720956
C 104	15.4	85.6	606	3	BM013427	C 177	15	83.3	206	1	AA353183
C 105	15.4	85.6	611	5	BO777182	C 178	15	83.3	209	9	BH311723
C 106	15.4	85.6	612	7	CK905521	C 179	15	83.3	213	1	AI434926
C 107	15.4	85.6	621	2	BB56765	C 180	15	83.3	215	1	AM103581
C 108	15.4	85.6	621	6	CD705000	C 181	15	83.3	217	7	CN260725
C 109	15.4	85.6	635	1	BM837637	C 182	15	83.3	225	1	AI1825290
C 110	15.4	85.6	636	5	BK477723	C 183	15	83.3	226	1	AA459415
C 111	15.4	85.6	640	8	CX182808	C 184	15	83.3	226	8	H25788
C 112	15.4	85.6	642	7	CK005791	C 185	15	83.3	228	2	BE018221
C 113	15.4	85.6	649	7	CK757899	C 186	15	83.3	230	1	AI654782
C 114	15.4	85.6	653	10	CE755366	C 187	15	83.3	233	1	AI866432
C 115	15.4	85.6	664	2	BZ144650	C 188	15	83.3	239	2	BI021689
C 116	15.4	85.6	669	2	BF965563	C 189	15	83.3	239	1	AA506757
C 117	15.4	85.6	674	5	BW957150	C 190	15	83.3	250	1	AA758370
C 118	15.4	85.6	685	10	AG157422	C 191	15	83.3	250	1	AA494208
C 119	15.4	85.6	686	8	DN151938	C 192	15	83.3	251	1	AA552063
C 120	15.4	85.6	696	2	BI861828	C 193	15	83.3	251	1	AA370233
C 121	15.4	85.6	716	2	BF673545	C 194	15	83.3	253	1	AA961889
C 122	15.4	85.6	725	10	AG438387	C 195	15	83.3	255	6	CF130444
C 123	15.4	85.6	749	5	BF678820	C 196	15	83.3	257	1	AM874594
C 124	15.4	85.6	788	5	BUS32673	C 197	15	83.3	257	3	H25782
C 125	15.4	85.6	789	9	BH588908	C 198	15	83.3	254	8	BP393561
C 126	15.4	85.6	792	11	CR108338	C 199	15	83.3	255	1	AI419779
C 127	15.4	85.6	809	9	CC358190	C 200	15	83.3	271	1	AA952963
C 128	15.4	85.6	813	5	BUS37587	C 201	15	83.3	271	2	BI021698
C 129	15.4	85.6	813	9	BH107451	C 202	15	83.3	275	1	AA878251
C 130	15.4	85.6	835	6	CA477721	C 203	15	83.3	275	1	AA532661
C 131	15.4	85.6	843	5	CC720645	C 204	15	83.3	282	1	AM015934
C 132	15.4	85.6	845	5	BK424436	C 205	15	83.3	284	2	BI089025
C 133	15.4	85.6	848	5	BQ431499	C 206	15	83.3	286	1	AM338581
C 134	15.4	85.6	857	11	CR079620	C 207	15	83.3	292	1	AI673126
C 135	15.4	85.6	858	9	BZ539723	C 208	15	83.3	292	1	AI673126
C 136	15.4	85.6	871	2	BF675225	C 209	15	83.3	293	1	AM068093
C 137	15.4	85.6	872	6	CD515594	C 210	15	83.3	305	1	AA502726
C 138	15.4	85.6	876	5	BU189739	C 211	15	83.3	311	3	BP385395
C 139	15.4	85.6	881	5	BK361165	C 212	15	83.3	314	3	BM768553
C 140	15.4	85.6	885	3	BO232385	C 213	15	83.3	315	1	AM516667
C 141	15.4	85.6	886	5	BK416924	C 214	15	83.3	318	1	AI278707
C 142	15.4	85.6	911	2	BK128031	C 215	15	83.3	318	1	AA508653
C 143	15.4	85.6	924	2	BE540523	C 216	15	83.3	318	2	BI021700
C 144	15.4	85.6	931	10	CM924982	C 217	15	83.3	322	1	AI248883
C 145	15.4	85.6	931	10	CG067841	C 218	15	83.3	322	5	EX473513
C 146	15.4	85.6	936	2	BF165108	C 219	15	83.3	330	1	AM591773
C 147	15.4	85.6	945	2	BG110396	C 220	15	83.3	334	1	AA506454
C 148	15.4	85.6	951	5	BO880107	C 221	15	83.3	337	7	T40539
C 149	15.4	85.6	951	10	CG921167	C 222	15	83.3	338	1	AM182773
C 150	15.4	85.6	1000	10	CG365229	C 223	15	83.3	338	1	AA479918
C 151	15.4	85.6	1015	5	BU272923	C 224	15	83.3	339	1	AI969104
C 152	15.4	85.6	1024	5	BG029496	C 225	15	83.3	339	2	BE908524
C 153	15.4	85.6	1046	6	CB961870	C 226	15	83.3	340	1	AI077915
C 154	15.4	85.6	1096	1	AL515292	C 227	15	83.3	342	2	BF939440
C 155	15.4	85.6	1120	1	AL535154	C 228	15	83.3	348	1	AI066019
C 156	15.4	85.6	1167	9	CC268116	C 229	15	83.3	348	1	AI523186
C 157	15.4	85.6	1303	8	DN685116	C 230	15	83.3	348	1	AA835477
C 158	15.4	85.6	1420	10	CL646896	C 231	15	83.3	350	1	AA835477
C 159	15.4	85.6	1453	4	AK051544	C 232	15	83.3	355	1	AA641534
C 160	15	83.3	125	1	AA938023	C 233	15	83.3	360	6	CA153872
C 161	15	83.3	128	1	AA285031	C 234	15	83.3	362	2	CG994684
C 162	15	83.3	134	8	W42749	C 235	15	83.3	363	1	AA953293
C 163	15	83.3	150	1	AI128633	C 236	15	83.3	363	1	AA484009
C 164	15	83.3	156	6	CD177653	C 237	15	83.3	364	1	AA473294
C 165	15	83.3	159	1	AA860424	C 238	15	83.3	367	1	AA665209
C 166	15	83.3	159	1	AA327953	C 239	15	83.3	370	2	BG752518
C 167	15	83.3	169	1	AA897049	C 240	15	83.3	371	2	BF058492
C 168	15	83.3	172	7	CN260722	C 241	15	83.3	371	8	W42436

AA151954	Z002901.8
AA559544	nm66c02.8
BI005692	RC4-HN017
AA481544	aa35905.8
BU670987	NISC 1r03
AA853831	NHTRBGA09
BG035839	602325931
EG035839	602325931
AI1720956	ab710709.x
AA353183	EST61302
BH311723	CH230-26H
AI434926	BI434926
AM103581	xe78h09.x
CN260725	170005999
AI828290	wa84h09.x
AA459415	xz89h05.8
H25788	y149b05.x.1
BE018221	bb77b07.y
AI654782	wb49902.x
AI866432	wk18c09.x
BI021689	CM3-MT034
AA506757	n113909.8
AA758370	z945901.8
AA494208	n999f08.8
AA552063	nk05d11.8
AA370233	EST81819
AA961889	or44d11.8
CF130444	UI-HF-BS0
AM874594	h06a12.x
H25782	y149a06.x.1
BZ393561	BP393561
AI419779	tg99e12.x
AA952963	CM3-C09.8
BI021698	CM3-MT034
AA878251	o104f05.8
AA532661	n145a03.8
AA514511	nf62c05.8
AM015934	UI-H-BI0P
BI089025	602853575
AM338581	xw72a10.x
AI673126	we71c01.x
AM068093	cn23b03.x
AA502726	nh57a03.8
BP385395	BP385395
BM768553	K-EST0051
AM516667	xq02d08.x
AI278707	qk60f11.x
AA508653	nh67906.8
AA506454	n11h10.8
T40539	y405d02.8.1
AM182773	xp97e08.x
AA479918	z444907.8
AI969104	w35907.x
BE908524	601501384
AI077915	oy15c11.8
BF939440	nad899G09.
AI066019	oy70f05.x
AI523186	at65908.x
AA835477	EST12940
AA641534	ak75a04.8
CA153872	SCVPR2203
BG994684	PM2-HT128
AA953293	oc74a04.8
AA484009	ne73f10.8
AA473294	xy23h07.x
AA665209	h18a07.x
BG752518	602731021
BF058492	7K31d07.x
W42436	z222d08.8.1

C 242	15	83.3	372.1	A13556935	OX21d07.x
C 243	15	83.3	372.2	AM070434	xa11b08.x
C 244	15	83.3	372.2	EG231838	BEG21fE02.
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C 246	15	83.3	374.1	AA550930	nj86d11.s
C 247	15	83.3	384.3	BM992970	UI-E-D70-
C 248	15	83.3	388.1	A1762657	w82E05.x
C 249	15	83.3	388.5	BX413818	EX413818
C 250	15	83.3	392.2	BG110552	BG110552
C 251	15	83.3	393.1	AI052485	AI052485
C 252	15	83.3	393.3	CR612702	AI219612.x
C 253	15	83.3	393.5	EX421021	CR612702
C 254	15	83.3	393.7	CN192912	EX421021
C 255	15	83.3	394.1	AI1222030	CN192912
C 256	15	83.3	397.1	AA699459	AI1222030
C 257	15	83.3	397.8	TS7831	AA699459
C 258	15	83.3	398.1	AA961603	TS7831
C 259	15	83.3	399.1	AI076417	AA961603
C 260	15	83.3	400.1	AI018107	AI076417
C 261	15	83.3	402.1	AA464265	AI018107
C 262	15	83.3	403.1	AI091825	AA464265
C 263	15	83.3	403.9	AQ118529	AI091825
C 264	15	83.3	405.1	AA806590	AQ118529
C 265	15	83.3	405.1	AA523728	AA806590
C 266	15	83.3	405.5	BU730512	AA523728
C 267	15	83.3	413.1	AI1299667	BU730512
C 268	15	83.3	413.1	AM263743	AI1299667
C 269	15	83.3	414.1	AA837993	AM263743
C 270	15	83.3	415.1	AI080097	AA837993
C 271	15	83.3	417.6	CF382840	AI080097
C 272	15	83.3	418.1	AI1248324	CF382840
C 273	15	83.3	420.1	AI1354517	AI1248324
C 274	15	83.3	420.8	N33480	AI1354517
C 275	15	83.3	421.1	AA065082	N33480
C 276	15	83.3	426.1	AI1744302	AA065082
C 277	15	83.3	427.7	CN137433	AI1744302
C 278	15	83.3	428.1	AI608877	CN137433
C 279	15	83.3	429.1	AA999919	AI608877
C 280	15	83.3	432.8	W86074	AA999919
C 281	15	83.3	433.1	AA723811	W86074
C 282	15	83.3	433.1	AA548418	AA723811
C 283	15	83.3	433.3	BM709842	AA548418
C 284	15	83.3	435.1	AI1445510	BM709842
C 285	15	83.3	435.2	BG2233171	AI1445510
C 286	15	83.3	437.1	AA458972	BG2233171
C 287	15	83.3	440.8	RS4623	AA458972
C 288	15	83.3	442.5	BU935555	RS4623
C 289	15	83.3	444.10	CE428666	BU935555
C 290	15	83.3	445.1	AI1446090	CE428666
C 291	15	83.3	447.1	AI0302723	AI1446090
C 292	15	83.3	448.1	AI1300503	AI0302723
C 293	15	83.3	454.1	AA291557	AI1300503
C 294	15	83.3	457.1	AA533309	AA291557
C 295	15	83.3	459.1	AI168496	AA533309
C 296	15	83.3	461.1	AI1761144	AI168496
C 297	15	83.3	461.8	N26709	AI1761144
C 298	15	83.3	462.5	BU734139	N26709
C 299	15	83.3	466.1	AI123437	BU734139
C 300	15	83.3	467.5	BU508676	AI123437
C 301	15	83.3	467.5	BU508676	BU508676

RESULT 1	BB629501	656 bp	mRNA	linear	EST 31-AUG-2001
LOCUS	BB629501				
DEFINITION	BB629501 RIKEN full-length enriched, adult male bone				Mus musculus
	cDNA clone 9830134F20 5', mRNA sequence.				
ACCESSION	BB629501				
VERSION	BB629501.1	GI:15399640			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				

ALIGNMENTS

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurionathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 656)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J.,
Komno,H., Kouda,M., Koya,S., Matuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sekai,C., Sekai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
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Matsubiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
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and Hayashizaki,Y.
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Komno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Yamanaka,I., Kiyosawa,H., Kondou,S., Saito,T., Shinagawa,A.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K.,
Arakawa,T., Ishii,Y. and Hayashizaki,Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Func. Genomics 2 pre, L72-L86 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.

location/Qualifiers
1. 656
/organism="Mus musculus"
/mol_type="cDNA"
/db_xref="taxon:10090"
/clone="9830134F20"
/sex="male"
/tissue_type="bone"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male bone"
/note="Site 1: Saliv. Site 2: Bambi, cDNA library was

contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGGAGAAGACATCCAAAGACTCTTTTTCCTTTTTTNN 3'], cDNA was prepared by using trehalose chemo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGGAGAAGTCTCGAGTTATTATTAATCCCCCCCC sequence [5', GAGGAGAAGTCTCGAGTTATTATTAATCCCCCCCC]. cDNA was cleaved with XhoI and BamHI. Vector: a

sequence [5' GAGAGAGAGATTCGAGTTAATTAATCCCCCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a

Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216).

cDNA library was prepared and sequenced in Mouse Genome Encyclopedic Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>.
URL: <http://fantom.gsc.riken.jp/>.
Location/Qualifiers

FEATURES

1. 2751
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM.DB:9830134F20"
/db_xref="taxon:10090"
/clone="9830134F20"
/sex="male"
/tissue_type="bone"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1. 2751
/note="kinase suppressor of ras (MGD) MGI:105051, GB|NM_013571, evidence: BLASTN, 100%, match=1985"

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 2751;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGGACCTTAGCGCAAG 18
|||||
345 CGGACCTTAGCGCAAG 362

Db 345 CGGACCTTAGCGCAAG 362

RESULT 5

CK370327/c CK370327 317 bp mRNA linear EST 23-DEC-2003
DEFINITION zmrw005.0A10-002-b11.80 zmrw005 Zea mays cDNA 5', mRNA sequence.

CK370327 CK370327.1 GI:40336257

KEYWORDS

SOURCE

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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Tel: 217-265-5475
Fax: 217-233-5574
Email: bohmert@life.uiuc.edu
POLY-A-No.

FEATURES

Location/Qualifiers

1. 317
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/clone_lib="zmrw005"
/note="Library zmrw005 consists of the same cDNA

material as library zmrw00 (described below) but was sequenced from the 5' primer end. The sequence identifier uses the '50' suffix because the library tag was at the 3' end and thus not identified. Samples were collected in Robert E. Sharp's lab (University of Missouri-Columbia) to construct three normalized cDNA libraries. Dark-grown maize seedlings with primary roots 12-20 mm in length were transplanted to high (-0.03 MPa) and low water potential (-1.6 MPa) vermiculite, and harvested at 5 h and 48 h after transplanting. About 1,000 roots were used for each of the low water potential libraries (zmrw05 and zmrw48) while 500 roots were combined from each of the two time points at high water potential (zmrw00). Each root was divided into 4 segments (distances are from the junction of the root apex and root cap): segment 1, 0-3 mm plus the root cap; segment 2, 3-7 mm; segment 3, 7-12 mm; segment 4, 12-20 mm. (For details of conditions see (1) with nutrient modifications as in (2)). The three normalized cDNA libraries were constructed in the lab of Hans Bohmert (University of Illinois-UC). Total RNA was extracted by the 'hot phenol' method (Plant Molecular Biology manual, DS: 1-13, 2nd ed., 1997). This method worked in eliminating carbohydrate material present in the root tips. The integrity of the RNA was verified by denaturing agarose gels and spectrophotometry (ratio A260/280). Poly(A)⁺mRNA was isolated twice from total RNA using the Oligotex Direct mRNA kit (Qiagen). Poly(A)⁺mRNA was converted to double-stranded cDNA and tagged by using modified Oligo(dT) primers. One of 4 sequence tags corresponding to a different segment of the root was added to the 3'-end of the modified Oligo(dT) primers, including a NotI site and used to reverse transcribe the segment-specific mRNAs into cDNAs. Each library contains all four tags. A suffix (s1, s2, s3, or s4) has been added to each sequence identifier to designate which region of the root (root segment 1, 2, 3, or 4) the sequence was found in based on the identification of the tag. A suffix of 80 indicates that the sequence tag, and hence the source segment, could not be identified. The double stranded cDNAs were size-selected (>450 bp). Size selected cDNAs were adsorbed with EcoRI adaptors at both ends, and then digested with NotI. The cDNA was directionally cloned into EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene) and electroporated into E. coli DH10B. The total number of white colony forming units (cfu) in the primary libraries before amplification was as follows: zmrw05: 3.37 x 10⁶; zmrw48: 4.87 x 10⁶; zmrw00: 3 x 10⁶. The background of empty clones was less than 1%. Inserts ranged from ~0.5 kb to >2.5 kb, as determined by PCR. Plasmid DNA from the primary libraries then was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming sites that flank the cloned cDNA inserts. The purified PCR products, representing the entire cDNA population cloned in each library, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 300C. Non-hybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B. The total number of clones with insert was: zmrw05: 2.0x10⁷; zmrw48: 4.2x10⁷; zmrw00: 1.1x10⁷. The background of empty clones was less than 2%. Insert size, determined by PCR of the entire library, ranged from 0.5 kb to 2.5 kb. (1) Sharp R E; Silk W K; Hsiao T C. Growth of the Maize Primary Root at Low Water Potentials I. Spatial Distribution of Expansive Growth. Plant Physiology (Rockville). 87(1). 1988. 50-57. (2) Spollen W G; Lenoble M E; Samuels T D; Bernstein N; Sharp R E. Abscissic acid accumulation maintains maize primary root elongation at low water potentials by restricting ethylene production. Plant Physiology (Rockville). 122(3). March,

ORIGIN

2000. 967-976.
TAG_TISSUE=Not found
TAG_SEQ=Not found"

Query Match 91.1%; Score 16.4; DB 7; Length 317;
Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18
41 CGGACCTAGAGGCAAG 24

RESULT 6
LOCUS CF633642 370 bp mRNA linear EST 02-OCT-2003
DEFINITION CF633642 zmrw00 0A10-002-b11.80 zmrw00 Zea mays cDNA 3', mRNA sequence.
ACCESSION CF633642 GI:37392777
VERSION CF633642.1
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
1 (bases 1 to 370)
Bohner, H., Sharp, R.E., Springer, G.K., Poroyko, V., Fredrickson, M.,
Clade, Panicoideae; Andropogoneae; Zea.
Sharp, R.E., Spollen, W.G., Ries, J., Guillen, A., Khambati, A.,
Topinka, C., Davis, G.E., Schachtman, D., Wu, Y., and Nguyen, H.T.
NSF Grant DBI-0211842: Functional Genomics of Root Growth and Root
Signaling Under Drought
Unpublished (2003)

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1201 West Gregory Drive, Urbana, IL 61801, USA
Tel: 217-265-5475
Fax: 217-333-5574
Email: bohner@life.uiuc.edu
POLYA=No.

FEATURES

source

Location/Qualifiers

1..370

/organism="Zea mays"

/mol_type="mRNA"

/db_xref="taxon:4577"

/clone_lib="zmrw00"

/note="Samples were collected in Robert E. Sharp's lab

(University of Missouri-Columbia) to construct three

normalized cDNA libraries. Dark-grown maize seedlings with

primary roots 12-20 mm in length were transplanted to high

(-0.03 MPa) or low water potential (-1.6 MPa) vermiculite,

and harvested at 5 h and 48 h after transplanting. About

1,000 roots were used for each of the low water potential

libraries (zmrw05 and zmrw48) while 500 roots were

combined from each of the two time points at high water

potential (zmrw00). Each root was divided into 4 segments

(distances are from the junction of the root apex and root

cap): segment 1, 0-3 mm plus the root cap; segment 2, 3-7

mm; segment 3, 7-12 mm; segment 4, 12-20 mm. (For details

of conditions see (1) with nutrient modifications as in

(2)). The three normalized cDNA libraries were constructed

in the lab of Hans Bohner (University of Illinois-UC).

Total RNA was extracted by the 'hot phenol' method (Plant

Molecular Biology manual, D5: 1-13, 2nd ed., 1997). This

method worked in eliminating carbohydrate material present

in the root tips. The integrity of the RNA was verified by

denaturing agarose gels and spectrophotometry (ratio

A260/A280). Poly(A)⁺ mRNA was isolated twice from total RNA

using the Oligotex Direct mRNA kit (Qiagen). Poly(A)⁺ mRNA

was converted to double-stranded cDNA and tagged by using

modified Oligo(dT) primers. One of 4 sequence tags

corresponding to a different segment of the root was added

to the 3'-end of the modified Oligo(dT) primers, including

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 370;
Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18
255 CGGACCTAGAGGCAAG 272

RESULT 7
LOCUS BE117998/c 510 bp mRNA linear EST 12-SEP-2000
DEFINITION PM1-HT0790-250600-001-809 HT0790 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE117998
VERSION BE117998.1 GI:10106263
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 510)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsumura, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

a NotI site and used to reverse transcribe the segment-specific mRNAs into cDNAs. Each library contains all four tags. A suffix (s1, s2, s3 or s4) has been added to each sequence identifier to designate which region of the root (root segment 1, 2, 3, or 4) the sequence was found in based on the identification of the tag. A suffix of s0 indicates that the sequence tag, and hence the source segment, could not be identified. The double stranded cDNAs were size-selected (>450 bp). Size selected cDNAs were adapted with EcoRI adaptors at both ends, and then digested with NotI. The cDNA was directionally cloned into EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene) and electroporated into E.coli DH10B. The total number of white colony forming units (cfu) in the primary libraries before amplification was as follows: zmrw05: 3.37 x 10⁶; zmrw48: 4.87 x 10⁶; zmrw00: 3 x 10⁶. The background of empty clones was less than 1%. Inserts ranged from ~0.5 kb to >2.5 kb, as determined by PCR. Plasmid DNA from the primary libraries then was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming sites that flank the cloned cDNA inserts. The purified PCR products, representing the entire cDNA population cloned in each library, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 30°C. Non-hybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B. The total number of clones with insert was: zmrw05: 2.0x10⁷; zmrw48: 4.2x10⁷; zmrw00: 1.1x10⁷. The background of empty clones was less than 2%. Insert size, determined by PCR of the entire library, ranged from 0.5 kb to 2.5 kb. (1) Sharp R.E., Silk W.K., Heislo T.C. Growth of the Maize Primary Root at Low Water Potentials I. Spatial Distribution of Expansive Growth. Plant Physiology (Rockville). 87(1). 1988. 50-57. (2) Spollen W.G., Lenoble M.E., Samuels T.D., Bernstein N., Sharp R.E. Absciseic acid accumulation maintains maize primary root elongation at low water potentials by restricting ethylene production. Plant Physiology (Rockville). 122(3). March, 2000. 967-976.
TAG_TISSUE=Not found
TAG_SEQ=Not found"

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

FEATURES
source
1..510
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0790"
/note="Organ: head neck; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
Location/Qualifiers
High quality sequence start: 20
High quality sequence stop: 429.

ORIGIN
Query Match 91.1%; Score 16.4; DB 2; Length 510;
Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 CGGACCTTAGGCAAG 18
443 CAGACCTTAGGCAAG 426

ORIGIN

RESULT 8
AG354283 704 bp DNA linear GSS 18-DEC-2004
LOCUS Mus musculus molossinus DNA, clone:MSMg01-152G07.T7, genomic survey
DEFINITION
sequence.
ACCESSION AG354283
VERSION AG354283.1 GI:47927593
KEYWORDS GSS
SOURCE Mus musculus molossinus (Japanese wild mouse)
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Abe, K., Noguchi, H., Tagawa, K., Yuzurika, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaki, K. and Shitohshi, T.
TITLE Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis
JOURNAL Genome Res. 14 (12), 2439-2447 (2004)
PUBMED 15574823
2 (bases 1 to 704)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
DIRECT SUBMISSION
TITLE Submitted (17-NOV-2003) Masahito Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suenho-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/)

COMMENT

Tel: 81-45-503-9111, Fax: 81-45-503-9170
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp

FEATURES
source
1..704
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-152G07.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

Query Match 91.1%; Score 16.4; DB 10; Length 704;
Best Local Similarity 94.4%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 CGGACCTTAGGCAAG 18
426 CGGACCTTAGGCAAG 443

ORIGIN
Query Match 91.1%; Score 16.4; DB 10; Length 704;
Best Local Similarity 94.4%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 CGGACCTTAGGCAAG 18
426 CGGACCTTAGGCAAG 443

ORIGIN

RESULT 9
DT058958 744 bp mRNA linear EST 11-AUG-2005
LOCUS AGENCOURT 55789292 NICHG_XGC_Fab Xenopus laevis cDNA clone
DEFINITION
IMAGE: 8069448 5', mRNA sequence.
ACCESSION DT058958
VERSION DT058958.1 GI:72358207
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Office of Cancer Genomics
Contact: Daniela S. Gerhard, Ph.D.
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: CGAPdb-rc@mail.nih.gov
Tissue Procurement: Tom Sargent
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM17342 row: d column: 22
High quality sequence stop: 623.
Location/Qualifiers
1..744
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:8069448"
/lab_host="DH10B Tona"

FEATURES

source
1..744
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:8069448"
/lab_host="DH10B Tona"

/clone_1lb="NICHD XGC Fab"
 /note="Organ: fat body; Vector: pExpress-1; Site_1: EcoRV;
 Site_2: NotI; cDNA was primed using oligo-dT primer:
 5'-pGACTAGTCTTAGATCGGAGCGGCCGCC(T)25-3' and cloned into
 the EcoRV/NotI sites of pExpress-1. Size-selection 1.2kb
 resulted in an average insert size of 1.8kb. This is a
 primary library (normalized library is NICHD XGC FabN) and
 was constructed by Express Genomics (Frederick, MD). Note:
 this is a (http://xgc.nci.nih.gov/) Xenopus Gene
 Collection library."

ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 744;
 Best Local Similarity 94.4%; Pred. No. 1.3e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 CGGACCTTAGAGGCAAG 18
 490 CGGACCTTAGAGGCAAG 507

RESULT 10 817 bp mRNA linear EST 04-FEB-2005
 LOCUS JGI CAAN2676.fwd NIH XGC tropic4 Xenopus tropicalis cDNA clone
 DEFINITION IMAGE:7688136 5', mRNA sequence.

ACCESSION CX910994
 VERSION CX910994.1 GI:58650338

SOURCE EST.
 ORGANISM Xenopus tropicalis (western clawed frog)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 Xenopodinae; Xenopus; Silurana.
 1 (bases 1 to 817)
 Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C.,
 Brokstein, P., and Lindquist, E.A.
 DOE Joint Genome Institute Xenopus tropicalis EST project
 Unpublished (2004)
 Other ESTs: JGI CAAN2676.rev
 Contact: Lindquist, E.A., Richardson, P.
 DOE Joint Genome Institute
 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 Tel: 925 296 5600
 Fax: 925 296 5710
 Email: cdna@jgi-psf.org
 Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
 University of California, Berkeley;
 http://tropicalis.berkeley.edu/home)
 cDNA Library Preparation: DOE Joint Genome Institute;
 http://www.jgi.doe.gov
 DNA Sequencing: DOE Joint Genome Institute; http://www.jgi.doe.gov
 Clone Distribution: I.M.A.G.E. Consortium/LLNL;
 http://image.llnl.gov
 Naming Conventions: EST name is generated by the concatenation of
 the JGI Clone id and the direction of sequencing. The suffix '.fwd'
 indicates a forward sequencing read of the insert. It does not
 necessarily reflect the orientation of the insert.
 Plate: CAAN 0025 row: h column: 22
 High quality sequence stop: 752.
 Location/Qualifiers

FEATURES

source 1..817
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="IMAGE:7688136"
 /sex="male"
 /tissue_type="Testes"
 /dev_stage="Adult"
 /lab_host="ElectroMAX DH10B"
 /clone_1lb="NIH XGC tropic4"
 /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
 This library was made from dt primed cDNA and cloned into

Invitrogen pCMVSPORT6 vector. The work was done at DOE
 Joint Genome Institute. Poly A RNA were primed with 5'
 GACTAGTCTTAGATCGGAGCGGCCGCC(T)25-3' and cloned into
 the EcoRV/NotI sites of pExpress-1. Size-selection 1.2kb
 resulted in an average insert size of 1.8kb. This is a
 primary library (normalized library is NICHD XGC FabN) and
 was constructed by Express Genomics (Frederick, MD). Note:
 this is a (http://xgc.nci.nih.gov/) Xenopus Gene
 Collection library."

ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 817;
 Best Local Similarity 94.4%; Pred. No. 1.3e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 CGGACCTTAGAGGCAAG 18
 132 CGGACCTTAGAGGCAAG 149

RESULT 11 875 bp mRNA linear EST 11-AUG-2005
 LOCUS DT058819/c
 DEFINITION AGENCOURT 55953048 NICHD XGC Fab Xenopus laevis cDNA clone
 IMAGE:8069448 3', mRNA sequence.

ACCESSION DT058819
 VERSION DT058819.1 GI:72358068

SOURCE EST.
 ORGANISM Xenopus laevis (African clawed frog)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 Xenopodinae; Xenopus; Xenopus.
 1 (bases 1 to 875)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Tom Sargent
 cDNA Library Preparation: Express Genomics
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLNL17342 row: d column: 22
 High quality sequence start: 479
 High quality sequence stop: 795.
 Location/Qualifiers

FEATURES

source 1..875
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="IMAGE:8069448"
 /lab_host="DH10B TONa"
 /clone_1lb="NICHD XGC Fab"
 /note="Organ: fat body; Vector: pExpress-1; Site_1: EcoRV;
 Site_2: NotI; cDNA was primed using oligo-dT primer:
 5'-pGACTAGTCTTAGATCGGAGCGGCCGCC(T)25-3' and cloned into
 the EcoRV/NotI sites of pExpress-1. Size-selection 1.2kb
 resulted in an average insert size of 1.8kb. This is a
 primary library (normalized library is NICHD XGC FabN) and
 was constructed by Express Genomics (Frederick, MD). Note:
 this is a (http://xgc.nci.nih.gov/) Xenopus Gene
 Collection library."

ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 875;
 Best Local Similarity 94.4%; Pred. No. 1.3e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CGACCTAGAGGCAAG 18
 Db 498 CGACCTAGAGGCAAG 481
 RESULT 12
 LOCUS BR247762 296 bp mRNA linear EST 06-JUL-2000
 DEFINITION BR247762 RIKEN full-length enriched, 7 days neonate cerebellum Mus
 musculus cDNA A730021A22 3', mRNA sequence.
 BR247762
 ACCESSION BR247762 GI:8940508
 VERSION
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS
 1 (bases 1 to 296)
 Komno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
 Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
 Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
 Iizawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
 Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Oda, H.,
 Okazaki, Y., Ono, T., Owa, C., Saito, H., Mizuno, Y., Nakamura, M., Oda, H.,
 Shibata, K., Shibata, Y., Shigemoto, Y., Shingawa, A., Shiraki, T.,
 Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A.,
 Takahashi, F., Tomioka, N., Toyota, T., Tsunoda, Y., Watanabe, S.,
 Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A.,
 Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and
 Hayashizaki, Y.
 RIKEN Mouse ESTs (Komno, H., et al.)
 unpublished (2000)
 TITLE
 JOURNAL
 COMMENT
 Contact: Yoshinori Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-reg@gscc.riken.jp, URL: http://genome.gsc.riken.jp/
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoaka, S.,
 Saeki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 The establishment and characterization of thermolabile enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Kusunagi, T., Akiyama, J., Shibata, K., Iizawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
 Okazaki, Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.
 FEATURES
 SOURCE
 1..296
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="A730021A22"
 /tissue_type="cerebellum"
 /dev_stage="7 days neonate"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 7 days neonate
 cerebellum"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken

contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTCTTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 20.0 and subtraction to Rot = 459.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGAGATCTCGAGTTATTTATTTATCCCTCCCCC
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a
 modified pBluescript KS(+) after bulk excision from lambda
 FLC I."

Query Match 88.9%; Score 16; DB 2; Length 296;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 CGACCTAGAGGCAAG 17
 Db 50 CGACCTAGAGGCAAG 65
 RESULT 13
 LOCUS BE768604/c 396 bp mRNA linear EST 20-SEP-2000
 DEFINITION QV2-F70010-090800-303-b06 F70010 Homo sapiens cDNA, mRNA sequence.
 BE768604
 ACCESSION BE768604.1 GI:10222262
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 396)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-27049222
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPER/P/LIC Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=at2-QV2-F70010-090
 800-303-b06&t3=2000-08-09&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 384.
 FEATURES
 SOURCE
 1..396
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="F70010"
 /note="Organ: prostate tumor; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORFESTS PCR (U.S. Letters Patent Application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under

ORIGIN low stringency conditions."

Query Match 88.9%; Score 16; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGACCTAGAGGCA 16
|||||
49 CGACCTAGAGGCA 34

RESULT 14

LOCUS A1762325 430 bp mRNA linear EST 20-DEC-1999
DEFINITION w97a04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2379150 3',
mRNA sequence.

ACCESSION A1762325
VERSION A1762325.1 GI:5177992
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 430)
NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.
Email: cgaps-rt@mail.nih.gov
Tissue Procurement: Christopher Moskalik, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LML at:
www.bio.11nl.gov/bdrp/image/image.html
Insert Length: 574 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 409.

FEATURES

Source

1. 430
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2379150"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: pTT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid11 was
prepared, and 96 circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(clonides 132376-132391, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Facima Bonaldo."

ORIGIN

Query Match 88.9%; Score 16; DB 1; Length 430;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACCTAGAGGCA 17
|||||
36 GGACCTAGAGGCA 21

RESULT 15

EM029828

LOCUS EM029828 507 bp mRNA linear EST 05-NOV-2001
DEFINITION 488200 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION EM029828
VERSION EM029828.1 GI:16743398
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 507)
Smith, T.P.L., Grose, M.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Case, E., Wray, J.E., White, J., Cho, J., Fahrkeny, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-Mckown, C.G., Petrea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keesle, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

TITLE Contact: Smith TPL
JOURNAL USDA, ARS, US Meat Animal Research Center
PUBMED PO Box 166, Clay Center, NE 68933-0166, USA
COMMENT Tel: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and mismatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCACATCAGCAGC
Plate: 118 row: A column: 17
Seq primer: ATTAGGTGACTACTAG.
Location/Qualifiers
1. 507
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus,
semiteendous muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

FEATURES

Source

1. 507
Location/Qualifiers
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus,
semiteendous muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

ORIGIN

Query Match 88.9%; Score 16; DB 3; Length 507;
Best Local Similarity 94.1%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTAGAGGCA 18
|||||
29 GGACCTAGAGGCA 45

RESULT 16
A1208178 538 bp mRNA linear EST 30-NOV-1998
LOCUS A1208178
DEFINITION g955a08.x1 Soares, teatis NHT Homo sapiens cDNA clone IMAGE:1839062
3' similar to gb:158603 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT
(HUMAN); mRNA sequence.

ACCESSION A1208178
VERSION A1208178.1 GI:3770120
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 538)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
 Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnlnl.gov/bdtp/image/image.html
 Insert length: 639 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 431.
 Location/Qualifiers

FEATURES
 source

```
1..538
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1839062"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis_NHT"
/notes="vector: pT7T3D-Pac (pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5']
TGTTACCATCTGAACTGAGAGCGCCGCCCAATTTTCTTTTCTTTT 3'}.
Double-stranded cDNA was ligated to Eco RI adaptors
(pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cots, and was
constructed by Bento Soares and M. Fatima Bonaldo."
```

ORIGIN

Query Match 88.9%; Score 16; DB 1; Length 538;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGACCTAGAGGCAAA 17
 |||||
 Db 528 GGACCTAGAGGCAAA 513

RESULT 17

AG498153 769 bp DNA linear GSS 22-DEC-2004
 LOCUS Mus musculus molossinus DNA, clone:MSMg01-397021.T7, genomic survey
 DEFINITION

ACCESSION AG498153
 VERSION AG498153.1 GI:48205383
 KEYWORDS GSS.
 SOURCE Mus musculus molossinus (Japanese wild mouse)
 ORGANISM Mus musculus molossinus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,
 Ezawa, K., Satou, N., Hattori, M., Sakaki, Y., Moriwaki, K. and
 Shioishi, T.
 Contribution of Asian mouse subspecies Mus musculus molossinus to
 genomic constitution of strain C57BL/6J, as defined by BAC-end
 sequence-SNP analysis
 Genome Res. 14 (12), 2439-2447 (2004)

TITLE

JOURNAL
 PUBMED
 15574823
 2 (bases 1 to 769)
 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
 Direct Submission
 Submitted (17-NOV-2003) Maehira Hattori, The Institute of Physical

COMMENT

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
 (E-mail: hattori@sc.riken.jp, URL: <http://hsp.gsc.riken.go.jp/>,
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 Clones are derived from the mouse BAC library MSMg01. For BAC
 library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
 Tsukuba Institute, Bio Resource Center.
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1
 Koyadai, Tsukuba, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@rtc.riken.jp

PRIMERS

Sequencing : T7
 LIBRARY : pBAC3.6
 Vector : EcoRI
 R.site 1 : EcoRI
 R.site 2 : EcoRI.

FEATURES**source**

```
1..769
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-397021.T7"
/sex="male"
/tissue="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
```

ORIGIN

Query Match 88.9%; Score 16; DB 10; Length 769;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACCTAGAGGCAAG 18
 |||||
 Db 160 GACCTAGAGGCAAG 175

RESULT 18

BE503972 123 bp mRNA linear EST 04-AUG-2000
 LOCUS h254a03.xl NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3211756 3',
 DEFINITION mRNA sequence.

ACCESSION BE503972
 VERSION BE503972.1 GI:9706380
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 123)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL, send email to:
info@image.lnlnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 104.
 Location/Qualifiers

REFERENCE

1 (bases 1 to 123)
 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
 Direct Submission
 Submitted (17-NOV-2003) Maehira Hattori, The Institute of Physical

JOURNAL

PUBMED
 15574823
 2 (bases 1 to 769)
 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
 Direct Submission
 Submitted (17-NOV-2003) Maehira Hattori, The Institute of Physical

FEATURES**source**

```
1..123
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
```


/clone="IMAGE:3211756"
 /tissue_type="carcinoid"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Lu24"
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI-CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonids 141920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 85.6%; Score 15.4; DB 2; Length 123;
 Best Local Similarity 94.1%; Pred. No. 3.6e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCTTAGAGGCAAG 18
 |||||
 51 GGACCTTAGAGGCCAAG 67

RESULT 19
 A1349272/c 143 bp mRNA linear EST 16-FEB-1999
 LOCUS ta75c07.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2049900 3',
 mRNA sequence.
 A1349272
 A1349272.1 GI:4086478
 EST.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE

1 (bases 1 to 143)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)

JOURNAL

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
 M.D., Ph.D.

CDNA Library Preparation: David B. Kitzman, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 236 Std Error: 0.00
 Seq primer: -40UP from Gibco.

FEATURES

source

Location/Qualifiers
 1. 143
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2049900"
 /tissue_type="stem cell 34+/38+"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP_HSC2"
 /note="Organ: bone marrow; Vector: PAMPI; mRNA made from bone marrow, stem cells 34+/38+, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 400 bp. Primary library, non-amplified."

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; Length 143;
 Best Local Similarity 94.1%; Pred. No. 3.7e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 GGACCTTAGAGGCAAG 18
 |||||
 58 GGACCTTAGAGGCCAAG 42

RESULT 20
 AA654607 170 bp mRNA linear EST 04-NOV-1997
 LOCUS ss99e02.g1 NCI_CGAP_Pc3 Homo sapiens cDNA clone IMAGE:1202810, mRNA
 sequence.
 AA654607
 AA654607.1 GI:2590761
 EST.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE

1 (bases 1 to 170)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)

JOURNAL
 COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui,
 M.D., Michael Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: David B. Kitzman, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40m13 fwd. Et from Amersham
 High quality sequence stop: 142.

FEATURES

source

Location/Qualifiers
 1. 170
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1202810"
 /sex="Male"
 /dev_stage="45 Years old"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP_Pc3"
 /note="Vector: PAMPI0; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was primed with oligo (dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into PAMPI0 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Kitzman."

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; Length 170;
 Best Local Similarity 94.1%; Pred. No. 3.8e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCTTAGAGGCAAG 18
 |||||
 65 GGACCTTAGAGGCCAAG 81

RESULT 21
 AA234751 177 bp mRNA linear EST 03-MAR-1997
 LOCUS AA234751

DEFINITION z38c05.s1 Soares NHPu_S1 Homo sapiens cDNA clone IMAGE:687464
3', mRNA sequence.

ACCESSION AA234751
AA234751.1 GI:1859468

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 177)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -41m3 fwd. ET from Amersham
High quality sequence stop: 157.
Location/Qualifiers

FEATURES
source 1..177
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5591614"
/db_xref="taxon:9606"
/clone="IMAGE:687464"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soares NHPu_S1"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not 1;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2bHM, pregnant uterus
NHPu, and fetal heart NHPu19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 26032-26523,
34088-345479, and 484488-489479."

ORIGIN
Query Match 85.6%; Score 15.4; DB 1; Length 177;
Best Local Similarity 94.1%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAAG 18
|||||
Db 53 GGACCTTAGAGGCAAG 69

RESULT 22
LOCUS A1099443 205 bp mRNA linear EST 20-AUG-1998
DEFINITION uc30f06.x1 Sugano mouse liver mla mus musculus cDNA clone
IMAGE:1481891.3', similar to SW:ALBU_Rat F02770 SERUM ALBUMIN
PRECURSOR. [1], mRNA sequence.

ACCESSION A1099443
A1099443.1 GI:3448968

VERSION EST.
KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 205)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Stepoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:930247
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source 1..205
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1481891"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse liver mla"
/note="Organ: liver; Vector: pME18S-Fl3; Site 1: DraIII
(CACTGCTG); Site 2: DraIII (CACTGCTG); 1st strand cDNA
was primed with an oligo (dT) primer
(ATCTGACCTTCTTTTCTTTT); double-stranded cDNA was
ligated to a DraIII adaptor (TGTGGCCCTGCTG), digested
and cloned into distinct DraIII sites of the pME18S-Fl3
vector (5' site CACTGCTG, 3' site CACTGCTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTTAAGCTGCG and 3' end
primer CGACTGCTGCTGAGCACA."

ORIGIN
Query Match 85.6%; Score 15.4; DB 1; Length 205;
Best Local Similarity 94.1%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGACCTTAGAGGCAAA 17
|||||
Db 27 CGATCCTTAGAGGCAAA 11

RESULT 23
LOCUS B1493189 215 bp mRNA linear EST 28-AUG-2001
DEFINITION d198e07.w1 Morton Fetal Cochlea Homo sapiens cDNA clone
IMAGE:2540629.3', mRNA sequence.

ACCESSION B1493189
B1493189.1 GI:15332533

VERSION EST.
KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 215)

AUTHORS

Robertson, N.G., Khetarpal, U., Gutierrez-Espeleta, G.A., Bieber, F.R. and Morton, C.C.

TITLE

Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening

JOURNAL

Genomics 23, 42-50 (1994)

COMMENT

7829101

Contact: Morton, C. C.

Departments of Pathology and Obstetrics, Gynecology and

Reproductive Biology

Brigham and Women's Hospital

75 Francis Street, Harvard Medical School, Boston, MA 02115, USA

Tel: 617 732 7980

Fax: 617 738 6996

Email: cmorton@rics.bwh.harvard.edu

DNA sequencing and analyses were performed by National Institutes

of Health Intramural Sequencing Center (NISC; see

<http://www.nisc.nih.gov>).

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Plate: LLM6328 row: 1 column: 14

Seq primer: T7 primer.

FEATURES

Location/Qualifiers

1..215

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2540629"

/tissue_type="cochlea"

/dev_stage="16-22 week fetus"

/lab_host="SOLR cells (kanamycin resistant)"

/clone_lib="Morton Fetal Cochlea"

/note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI;

Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned

unidirectionally. Primer: Oligo dt. Fetal cochlea, normal.

37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP

XR Vector Library constructed by N. Robertson, C. Morton.

-5' adaptor sequence: 5' GAATTCGACACAG 3' -3' adaptor

sequence: 5' CTCGAGTTTCTTTTCTTTT 3' "

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 215;

Best Local Similarity 94.1%; Pred. No. 3.8e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAAG 18

|||||

28 GGACCTTAGAGGCAAG 44

Db

RESULT 24

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..241

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-236H6"

/sex="Male"

/cell_type="Spleen/Brain"

/clone_lib="RPCI-24"

/note="Vector: pTARBA1; Site 1: BamHI; Site 2: BamHI;

RPCI-24 Mouse BAC Library produced by Pieter de Jong. The

library was cloned in the pTARBA1 cloning vector at the

BamHI sites using MboI partially digested male C57BL/6J

DNA."

Seq primer: M13R1 reverse primer (ABI).

Location/Qualifiers

1..241

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-236H6"

/sex="Male"

/cell_type="Spleen/Brain"

/clone_lib="RPCI-24"

/note="Vector: pTARBA1; Site 1: BamHI; Site 2: BamHI;

RPCI-24 Mouse BAC Library produced by Pieter de Jong. The

library was cloned in the pTARBA1 cloning vector at the

BamHI sites using MboI partially digested male C57BL/6J

DNA."

Seq primer: M13R1 reverse primer (ABI).

Location/Qualifiers

1..241

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-236H6"

/sex="Male"

/cell_type="Spleen/Brain"

/clone_lib="RPCI-24"

/note="Vector: pTARBA1; Site 1: BamHI; Site 2: BamHI;

RPCI-24 Mouse BAC Library produced by Pieter de Jong. The

library was cloned in the pTARBA1 cloning vector at the

BamHI sites using MboI partially digested male C57BL/6J

DNA."

Seq primer: M13R1 reverse primer (ABI).

Location/Qualifiers

1..241

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-236H6"

/sex="Male"

/cell_type="Spleen/Brain"

/clone_lib="RPCI-24"

/note="Vector: pTARBA1; Site 1: BamHI; Site 2: BamHI;

RPCI-24 Mouse BAC Library produced by Pieter de Jong. The

library was cloned in the pTARBA1 cloning vector at the

BamHI sites using MboI partially digested male C57BL/6J

DNA."

Seq primer: M13R1 reverse primer (ABI).

Location/Qualifiers

1..241

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-236H6"

/sex="Male"

/cell_type="Spleen/Brain"

/clone_lib="RPCI-24"

/note="Vector: pTARBA1; Site 1: BamHI; Site 2: BamHI;

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DNA."

Seq primer: M13R1 reverse primer (ABI).

Location/Qualifiers

1..241

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-236H6"

/sex="Male"

/cell_type="Spleen/Brain"

/clone_lib="RPCI-24"

/note="Vector: pTARBA1; Site 1: BamHI; Site 2: BamHI;

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DNA."

Seq primer: M13R1 reverse primer (ABI).

Location/Qualifiers

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/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-236H6"

/sex="Male"

/cell_type="Spleen/Brain"

/clone_lib="RPCI-24"

/note="Vector: pTARBA1; Site 1: BamHI; Site 2: BamHI;

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Seq primer: M13R1 reverse primer (ABI).

Location/Qualifiers

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/mol_type="genomic DNA"

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/db_xref="taxon:10090"

/clone="RPCI-24-236H6"

/sex="Male"

/cell_type="Spleen/Brain"

/clone_lib="RPCI-24"

/note="Vector: pTARBA1; Site 1: BamHI; Site 2: BamHI;

RPCI-24 Mouse BAC Library produced by Pieter de Jong. The

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DNA."

Seq primer: M13R1 reverse primer (ABI).

Location/Qualifiers

1..241

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-236H6"

/sex="Male"

/cell_type="Spleen/Brain"

/clone_lib="RPCI-24"

/note="Vector: pTARBA1; Site 1: BamHI; Site 2: BamHI;

RPCI-24 Mouse BAC Library produced by Pieter de Jong. The

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DNA."

Seq primer: M13R1 reverse primer (ABI).

Location/Qualifiers

1..241

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-236H6"

/sex="Male"

/cell_type="Spleen/Brain"

/clone_lib="RPCI-24"

/note="Vector: pTARBA1; Site 1: BamHI; Site 2: BamHI;

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DNA."

Seq primer: M13R1 reverse primer (ABI).

Location/Qualifiers

1..241

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-236H6"

/sex="Male"

/cell_type="Spleen/Brain"

/clone_lib="RPCI-24"

/note="Vector: pTARBA1; Site 1: BamHI; Site 2: BamHI;

RPCI-24 Mouse BAC Library produced by Pieter de Jong. The

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DNA."

Seq primer: M13R1 reverse primer (ABI).

Location/Qualifiers

1..241

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-236H6"

/sex="Male"

/cell_type="Spleen/Brain"

/clone_lib="RPCI-24"

/note="Vector: pTARBA1; Site 1: BamHI; Site 2: BamHI;

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Seq primer: M13R1 reverse primer (ABI).

Location/Qualifiers

1..241

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-236H6"

/sex="Male"

/cell_type="Spleen/Brain"

/clone_lib="RPCI-24"

/note="Vector: pTARBA1; Site 1: BamHI; Site 2: BamHI;

RPCI-24 Mouse BAC Library produced by Pieter de Jong. The

library was cloned in the pTARBA1 cloning vector at the

BamHI sites using MboI partially digested male C57BL/6J

DNA."

source

1. .258

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2540629"

/tissue_type="cochlea"

/dev_stage="16-22 week fetus"

/lab_host="SOLR cells (kanamycin resistant)"

/clone_1ib="Morton Fetal Cochlea"

/note="Organ: ear; Vector: pBluescript SK-; Site 1: EcorI; Site 2: XhoI; Reference: Genomics 23, 42-50, (1994) Cloned unidirectionally. Primer: Oligo dt. Fetal cochlea, normal. 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP XR Vector. Library constructed by N. Robertson, C. Morton. ~5' adaptor sequence: 5' GAATTCGGCAGCAG 3' ~3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3' "

Query Match 85.6%; Score 15.4; DB 3; Length 258;

Best Local Similarity 94.1%; Pred. No. 3.9e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18

DB 188 GGACCTAGAGGCAAG 172

RESULT 26

LOCUS BG384534/ 288 bp mRNA linear EST 12-MAR-2001

DEFINITION BG384534 303762 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.

ACCESSION BG384534

VERSION BG384534.1 GI:13309078

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Sus.

1 (bases 1 to 288)

Fahnenkirk, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Petrea, G., Sultana, R., Quackenbush, J., and Keese, U.W.

Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly

Mamm. Genome 13 (8), 475-478 (2002)

12226715

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smtth@mail.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -mismatches 18 and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGCTACGAG

Plate: 92 row: B column: 1

Seq primer: ATTGAGTGACACTATG.

Location/Qualifiers

1. .288

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/tissue_type="pooled"

/lab_host="DHI08"

/clone_1ib="MARC 1P1G"

/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."

ORIGIN

Query Match 85.6%; Score 15.4; DB 2; Length 288;

Best Local Similarity 94.1%; Pred. No. 3.9e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18

DB 77 GGACCTAGAGGCAAG 61

RESULT 27

LOCUS AA746945 295 bp mRNA linear EST 16-JAN-1998

DEFINITION AA746945 1662105.81 NCI CGAP Alvi1 Homo sapiens cDNA clone IMAGE:1266873, mRNA sequence.

ACCESSION AA746945

VERSION AA746945.1 GI:2786903

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 295)

NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Kitzman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: www.bio.lim.gov/bdrip/image/image.html

Seq primer: -40ml3 fwd. RT from Amersham.

Location/Qualifiers

1. .295

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1266873"

/tissue_type="alveolar rhabdomyosarcoma"

/lab_host="DHI08"

/clone_1ib="NCI CGAP Alvi1"

/note="Vector: pAMP10; mRNA made from alveolar rhabdomyosarcoma, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Kitzman et al. (1996) Cancer Research 56:5380-5383."

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; Length 295;

Best Local Similarity 94.1%; Pred. No. 4e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18

DB 62 GGACCTAGAGGCAAG 78

RESULT 28

LOCUS AA747067 296 bp mRNA linear EST 07-FEB-1998

DEFINITION AA747067 1665411.81 NCI CGAP Alvi1 Homo sapiens cDNA clone IMAGE:1267125, mRNA sequence.

ACCESSION AA747067

VERSION AA747067.1 GI:2787025

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 296)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrrp/image/image.html
Insert Length: 371 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.
Location/Qualifiers
1..296
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1267125"
/tissue_type="alveolar rhabdomyosarcoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Alve1"
/note="Vector: pAMP10; mRNA made from alveolar
rhabdomyosarcoma, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp. Reference: Krizman et al.
(1996) Cancer Research 56:5380-5383."

ORIGIN
Query Match 85.6%; Score 15.4; DB 1; Length 296;
Best Local Similarity 94.1%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCTAGAGGCAAG 18
|||||
62 GGACCTAGAGGCCAAG 78
|||||

RESULT 29
LOCUS AM087244 313 bp mRNA linear EST 15-OCT-1999
DEFINITION X097c11.x1 NCI CGAP Co21 Homo sapiens cDNA clone IMAGE:2582708 3',
mRNA sequence.
ACCESSION AM087244
VERSION AM087244.1 GI:6043049
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 313)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskajuk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

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www-bio.llnl.gov/bdrrp/image/image.html
Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 301.
Location/Qualifiers
1..313
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2582708"
/tissue_type="moderately differentiated adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Co21"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; cloned unidirectionally. Primer: Oligo dT.
Normalized to Cot >500. Average insert size 1.04kb.
Normalized version of NCI-CGAP Co18. Library constructed
by Life Technologies."

ORIGIN
Query Match 85.6%; Score 15.4; DB 1; Length 313;
Best Local Similarity 94.1%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCTAGAGGCAAG 18
|||||
270 GGATCCTAGAGGCAAG 254
|||||

RESULT 30
LOCUS BM743266 326 bp mRNA linear EST 01-MAR-2002
DEFINITION K-EST0016364 S4SNUI Homo sapiens cDNA clone S4SNUI-10-E01 5', mRNA
sequence.
ACCESSION BM743266
VERSION BM743266.1 GI:19064595
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 326)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, D.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@mail.kribb.re.kr
Plate: 10 row: E column: 01
High quality sequence stop: 326.
Location/Qualifiers
1..326
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S4SNUI-10-E01"
/sex="M"
/tissue_type="Stomach"
/cell_type="Lymphoblast-like"
/cell_line="SNU-1"
/lab_host="Top10F"
/clone_lib="S4SNUI"
/note="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then dephosphorylated with

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with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 326;
 Best Local Similarity 94.1%; Pred. No. 4e+03; 1; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 1;

Oy 2 GGACCTAGAGGCAAG 18
 |||||
 Db 115 GGACCTAGAGGCAAG 99

Search completed: April 15, 2006, 18:51:14
 Job time : 3827 secs